

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:07:03 ; Search time 100.009 Seconds
(without alignments)
2909.975 Million cell updates/sec

Title: US-09-856-681A-2
Perfect score: 5450
Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5450	100.0	1030	3	AAY71460	Aay71460 Human sem
2	5371.5	98.6	1047	6	ADA23362	Ada23362 Human SEC
3	5103.5	93.6	975	4	AAB90731	Aab90731 Human CJ1
4	5088	93.4	974	2	AAW64221	Aaw64221 Human sec
5	4921	90.3	939	3	AAB23030	Aab23030 Human sem
6	4921	90.3	939	6	ADA23281	Ada23281 Human SEC
7	4590.5	84.2	884	3	AAB23031	Aab23031 Human sem
8	4590.5	84.2	884	6	ADA23283	Ada23283 Human SEC
9	3677	67.5	699	4	AAB95139	Aab95139 Human pro

10	3373	61.9	630	3	AAB23043	Aab23043	Human	sem
11	3373	61.9	630	6	ADA23307	Ada23307	Human	SEC
12	3362	61.7	626	6	ADA23360	Ada23360	Human	SEC
13	2980.5	54.7	574	4	AAB95317	Aab95317	Human	pro
14	2952	54.2	562	4	AAB94104	Aab94104	Human	pro
15	2947	54.1	562	4	AAM93444	Aam93444	Human	pol
16	2891	53.0	863	4	ABG04066	Abg04066	Novel	hum
17	2879.5	52.8	962	4	ABG04620	Abg04620	Novel	hum
18	2621.5	48.1	507	4	AAB92688	Aab92688	Human	pro
19	2361.5	43.3	1086	4	AAG63213	Aag63213	Amino	aci
20	2349.5	43.1	1088	5	ABG79177	Abg79177	Human	sem
21	2346	43.0	1017	5	AAG79413	Aag79413	CADHP-2,	
22	2335	42.8	1035	5	ABG79173	Abg79173	Human	sem
23	2326.5	42.7	1032	5	ABG79175	Abg79175	Human	sem
24	2213	40.6	418	4	AAB95886	Aab95886	Human	pro
25	2013.5	36.9	888	2	AAW19857	Aaw19857	Human	sem
26	2009.5	36.9	888	3	AAB18916	Aab18916	A novel	p
27	2009.5	36.9	888	4	AAU12443	Aau12443	Human	PRO
28	2009.5	36.9	888	5	ABB84950	Abb84950	Human	PRO
29	2009.5	36.9	888	5	ABB95556	Abb95556	Human	ang
30	2009.5	36.9	888	6	ABO17887	Abo17887	Novel	hum
31	2009.5	36.9	888	6	ABU69110	Abu69110	Human	PRO
32	2009.5	36.9	888	6	ABU81141	Abu81141	Human	PRO
33	2009.5	36.9	888	6	ABO19426	Abo19426	Human	sec
34	2009.5	36.9	888	6	ABU66841	Abu66841	Human	PRO
35	2009.5	36.9	888	6	ABU59922	Abu59922	Novel	sec
36	2009.5	36.9	888	6	ABU69087	Abu69087	Human	PRO
37	2009.5	36.9	888	6	ABO25112	Abo25112	Human	sec
38	2009.5	36.9	888	6	ABU67117	Abu67117	Human	sec
39	2009.5	36.9	888	6	ABU81551	Abu81551	Human	sec
40	2009.5	36.9	888	6	ADA46063	Ada46063	Novel	hum
41	2009.5	36.9	888	6	ADA76560	Ada76560	Novel	hum
42	2009.5	36.9	888	6	ADA76494	Ada76494	Human	PRO
43	2009.5	36.9	888	6	ADA19144	Ada19144	Human	PRO
44	2009.5	36.9	888	6	ADA61767	Ada61767	Homo sapi	
45	2009.5	36.9	888	6	ADB19552	Adb19552	Novel	hum

ALIGNMENTS

RESULT 1

AAAY71460

ID AAY71460 standard; protein; 1030 AA.

XX

AC AAY71460;

XX

DT 04-OCT-2000 (first entry)

XX

DE Human semaphorin 6A-1.

XX

KW Human; semaphorin 6A-1; (HSA)SEMA6A-1; neuronal development; apoptosis;

KW neuronal regeneration; Ena/VASP protein family; immunomodulatory;

KW gene therapy; diagnostic agent; therapeutic agent; differentiation;

KW cytoskeletal stabilisation; plasticity.

XX

OS Homo sapiens.

```

XX      Key                Location/Qualifiers
FH      Binding-site      957. .961
FT                                           /note= "Specific binding motif for members of Ena/VASP
FT                                           protein family, especially Evl"
FT      Binding-site      959. .1030
FT                                           /note= "Zyxin-like domain that selectively binds to
FT                                           members of Ena/VASP protein family, especially Evl"
FT      Binding-site      1009. .1014
FT                                           /note= "Specific binding motif for members of Ena/VASP
FT                                           protein family, especially Evl"
XX
PN      WO200031252-A1.
XX
PD      02-JUN-2000.
XX
PF      26-NOV-1999;      99WO-EP009215.
XX
PR      26-NOV-1998;      98EP-00122441.
XX
PA      (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI      Behl C,  Klostermann A;
XX
DR      WPI; 2000-400065/34.
DR      N-PSDB; AAD01233.
XX
PT      Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent,
PT      therapeutic agent, for modulating immune system, in gene therapy or for
PT      effecting differentiation, cytoskeletal stabilization and/or plasticity.
XX
PS      Example 1; Page 29-33; 53pp; English.
XX
CC      The present sequence is a transmembranous human semaphorin 6A-1
CC      ((HSA)SEMA6A-1) which is involved in neuronal development and
CC      regeneration mechanisms during apoptosis. Semaphorin is a family of
CC      proteins displaying secreted or transmembrane-based repulsive guidance
CC      cues critically involved in neuronal development. The present sequence
CC      was isolated from human 1-ZAP Express cDNA library which was screened
CC      using a PCR fragment amplified from human neuroblastoma cell line SK-N-MC
CC      cDNA. The (HSA)SEMA6A-1 protein contains a Zyxin-like domain that
CC      selectively binds to members of Ena/VASP protein family especially Evl.
CC      Expression of (HSA)SEMA6A-1 is highest in embryonic brain and kidney and
CC      moderate in lung. The present sequence is useful as diagnostic and
CC      therapeutic agents, for modulating the immune system, in gene therapy,
CC      for effecting differentiation, cytoskeletal stabilisation and plasticity
XX
SQ      Sequence 1030 AA;

Query Match                100.0%;  Score 5450;  DB 3;  Length 1030;
Best Local Similarity      100.0%;  Pred. No. 0;
Matches 1030;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
      |||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKOYPVFVGHKPGRNTTORHRLDIOM 60

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Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF	120
Db	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Db	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Db	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGG	540
Db	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR	600
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR	600
Qy	601	GGMLDWKHL LDSPDSTDPLGAVSSH NHQDKKGVIRESYLK GHDQLVPV TLLAIAVILAFV	660
Db	601	GGMLDWKHL LDSPDSTDPLGAVSSH NHQDKKGVIRESYLK GHDQLVPV TLLAIAVILAFV	660
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPE	720
Db	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPE	720
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ	840
Db	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ	840
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Qy	901	SKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTN SSNSSHL SRNQSFGRGDNPP	960


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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 SKRLEMHSSSYGVDYKRSYPTNSLTRSHQATTLLKRNNTNSSNSSHLNRNQSFGRGDNPP 960
Qy      961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS 1020
Qy      1021 TSMKPNDACT 1030
          ||||||||||
Db      1021 TSMKPNDACT 1030

```

RESULT 2

ADA23362

ID ADA23362 standard; protein; 1047 AA.

XX

AC ADA23362;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide, SEC15.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;

KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;

KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;

KW cardiovascular disease; oncology disease; immune disorder;

KW autoimmune disease; transplant rejection; allergy; AIDS; infections;

KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;

KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;

KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;

KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;

KW antiallergic; cardiant; dermatological.

XX

OS Homo sapiens.

XX

PN US2003054514-A1.

XX

PD 20-MAR-2003.

XX

PF 19-SEP-2001; 2001US-00957187.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 04-JAN-2000; 2000US-0174485P.

PR 08-MAR-2000; 2000US-00520781.

PR 19-SEP-2000; 2000US-0233798P.

PR 20-SEP-2000; 2000US-0234082P.

XX

PA (SHIM/) SHIMKETS R A.

PA (LARO/) LAROCHELLE W J.

XX

PI Shimkets RA, Larochelle WJ;

XX

DR WPI; 2003-540616/51.

DR N-PSDB; ADA23361.

XX

PT New SECX nucleic acids, useful for treating or diagnosing a disorder

PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.

XX

PS Claim 12; Page 14; 118pp; English.

XX

CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence represents a
CC SECX polypeptide of the invention.

XX

SQ Sequence 1047 AA;

Query Match 98.6%; Score 5371.5; DB 6; Length 1047;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1023; Conservative 0; Mismatches 7; Indels 17; Gaps 1;

```
Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
          |||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SHCNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS RQADV DTCRMKGKHKDECHNF 120
          |||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS RQADV DTCRMKGKHKDECHNF 120

Qy    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
          |||
Db    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240
          |||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
          |||
Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
          |||
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVGTGRFKEQKSPDSTWTPVPDER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
          |||
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
          |||
Db    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480

Qy    481 GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG 540
```

Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKBPLGRDERHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSL	583
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTFLPDNEMSYNTVYGHSSSL	600
Qy	584	PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSSHNHQDKKGVIRESYLKGH	643
Db	601	PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSSHNHQDKKGVIRESYLKGH	660
Qy	644	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	703
Db	661	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	720
Qy	704	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	763
Db	721	KLSGLFGDTWSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	780
Qy	764	LQQKRKPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQ	823
Db	781	LQQKRKPSRGSREWERNQNINACTKDMPPMGSPVIPTCLPLRASPSHIPSVVVLPIITQQ	840
Qy	824	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	883
Db	841	BYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	900
Qy	884	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRNTNSSN	943
Db	901	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRNTNSSN	960
Qy	944	SSHLNRNQSFGRGDNPPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961	SSHLNRNQSFGRGDNPPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
Qy	1004	PSLKPDPVPPKPSFAPLSTSMKPNDACT	1030
Db	1021	PSLKPDPVPPKPSFAPLSTSMKPNDACT	1047

RESULT 3

AAB90731

ID AAB90731 standard; protein; 975 AA.

XX

AC AAB90731;

XX

DT 07-JUN-2001 (first entry)

XX

DE Human CJ145_1 protein sequence SEQ ID 161.

XX

KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
KW differentiation; immune system modulator; tissue growth; chemotactic;
KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
KW haematopoiesis.

XX

OS Homo sapiens.

XX

PN WO200119988-A1.
 XX
 PD 22-MAR-2001.
 XX
 PF 14-SEP-2000; 2000WO-US025135.
 XX
 PR 17-SEP-1999; 99US-00398829.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
 XX
 DR WPI; 2001-244801/25.
 DR N-PSDB; AAF98469.
 XX
 PT Isolated nucleic acids encoding polypeptides, useful for modulating e.g.
 PT cytokine and cell proliferation/differentiation activity, the immune
 PT system and hematopoiesis regulating activity.
 XX
 PS Disclosure; Page 487-490; 557pp; English.
 XX
 CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;
 CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis
 CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition
 CC activity. Included in the invention are probes represented in AAF98490 -
 CC AAF98572 which are specific for the cDNA clones encoding the secreted
 CC proteins
 XX
 SQ Sequence 975 AA;

Query Match 93.6%; Score 5103.5; DB 4; Length 975;
 Best Local Similarity 94.4%; Pred. No. 0;
 Matches 972; Conservative 0; Mismatches 3; Indels 55; Gaps 1;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRN TTQRHRLDIQM 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRN TTQRHRLDIQM 60

 Qy 61 IMIMNGTLYIAARDHIYTV DIDSHT EEEIYCSKKLTWKS RQADV DTCRMKGKHKDECHNF 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 IMIMNGTLYIAARDHIYTV DIDSHT EEEIYCSKKLTWKS RQADV DTCRMKGKHKDECHNF 120

 Qy 121 IKVLLKKND DALFVCGTNAFNP SCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 IKVLLKKND DALFVCGTNAFNP SCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

 Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYG DYIYFFFREIA 240

Db	181	 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVTVFLGSEKGIILKFLARIGNSGFLNDSLFLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVTVFLGSEKGIILKFLARIGNSGFLNDSLFLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWKEGG	540
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	576
Qy	601	GGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLKGHDQLVPVTLIAIAVILAFV	660
Db	577	-----GVIRESYLKGHDQLVPVTLIAIAVILAFV	605
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPE	720
Db	606	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPE	665
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	666	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	725
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	840
Db	726	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	785
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	786	MALEDQAATLEYKTIKEHFSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLFQTGL	845
Qy	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPP	960
Db	846	SKRLEMHHSFSYGVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPP	905
Qy	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	1020
Db	906	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	965
Qy	1021	TSMKPNDACT	1030

RESULT 4

AAW64221

ID AAW64221 standard; protein; 974 AA.

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AC AAW64221;

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DT 06-OCT-1998 (first entry)

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DE Human secreted protein from clone CJ145_1.

XX

KW Secreted protein; human fetal brain; nutrition; cytokine; stimulant;
KW cell proliferation; differentiation; immune system; suppressor; ligand;
KW regulator; hematopoiesis; tissue growth; activin; inhibin; haemostatic;
KW chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;
KW anti-inflammatory.

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OS Homo sapiens.

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PN WO9827205-A2.

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PD 25-JUN-1998.

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PF 17-DEC-1997; 97WO-US023330.

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PR 18-DEC-1996; 96US-00769192.

PR 13-JAN-1997; 97US-00783401.

PR 16-DEC-1997; 97US-00991872.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;

XX

DR WPI; 1998-362774/31.

DR N-PSDB; AAV44295.

XX

PT New polynucleotides and secreted proteins - obtained from human foetal
PT brain, human adult testes, human adult brain and human adult salivary
PT gland cDNA libraries.

XX

PS Claim 17j; Page 71-74; 110pp; English.

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CC This sequence represents a novel secreted protein from clone CJ145_1
CC isolated from a human fetal brain cDNA library. This protein has
CC applications for nutritional use, cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, hematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombotic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity and other activities

XX

SQ Sequence 974 AA;

Query Match 93.4%; Score 5088; DB 2; Length 974;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 971; Conservative 0; Mismatches 3; Indels 56; Gaps 2;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNNTQRHRLDIQM	60
Db	1	MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNNTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
Db	61	IMIMNGTLYIAARDHIYTVDIDTSH-EEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	119
Qy	121	IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Db	120	IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	179
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Db	180	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	239
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	240	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	299
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	300	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	359
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRRL	420
Db	360	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRRL	419
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	420	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	479
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWKEGG	540
Db	480	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWKEGG	539
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR	600
Db	540	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	575
Qy	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPVTLTLLAIAVILAFV	660
Db	576	-----GVIRESYLKGHDLVPVTLTLLAIAVILAFV	604
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	605	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE	664
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	665	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	724
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQ	840

Db	725	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	784
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	785	MALEDQAATLEYKTIKEHFSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLFQTGL	844
Qy	901	SKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNTNSSNSSHLNRNQSFGRGDNPP	960
Db	845	SKRLEMHHSSFSYGVYDKRSYPTNSLTRSHQATTLKRNTNSSNSSHLNRNQSFGRGDNPP	904
Qy	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS	1020
Db	905	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS	964
Qy	1021	TSMKPNDACT	1030
Db	965	TSMKPNDACT	974

RESULT 5

AAB23030

ID AAB23030 standard; protein; 939 AA.

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AC AAB23030;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant, SECX 2864933-1.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy.

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OS Homo sapiens.

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PN WO200053742-A2.

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PD 14-SEP-2000.

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PF 09-MAR-2000; 2000WO-US006280.

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PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR N-PSDB; AAA93617.

PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.

XX

PS Claim 1; Fig 2; 151pp; English.

XX

Sequences AAB23029-B23048 represent human SECX proteins. The SECX proteins of the invention are either secreted or membrane-associated proteins and act as regulator of cellular proliferation and differentiation. SECX proteins or nucleotides are useful for diagnosing the presence of, or predisposition to, a disease associated with altered levels of SECX proteins and nucleotides. The SECX proteins are also useful to screen compounds that modulate SECX activity or expression. The interaction of a SECX protein with other cellular proteins may be useful to modulate the activity of a partner protein, cellular proliferation, cellular differentiation and cell survival. SECX nucleotides are useful for the recombinant expression of SECX protein, and may be used detect SECX mRNA or genetic lesions in the SECX gene. They may also be used to modulate SECX expression (e.g., using antisense oligonucleotides). SECX nucleic acid sequences are also useful for identifying a cell or tissue type in a biological sample, and in forensic biology. SECX primers or probes are useful for detecting the presence of SECX nucleotides and for screening tissue cultures for contamination. Diseases that may be treated or prevented using SECX proteins or nucleotides include cancer (e.g., colorectal carcinoma, prostate cancer), benign tumours, immune disorders (including autoimmune diseases, transplant rejection, allergies, AIDS), infections, inflammatory disorders, arthritis, haematopoietic disorders, skin disorders, cardiovascular disorders, atherosclerosis, restenosis, neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 939 AA;

Query Match 90.3%; Score 4921; DB 3; Length 939;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 928; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

90.3%; Score 4921; DB 3; Length 939;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 928; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	5
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Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Ov 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	5
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Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120

OY 121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Db 121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Ov 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

|||||

Db 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

QV 241 VEYNTMGKVVFPRVAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG	540
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600
Qy	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQQKKGVIRESYLKGHDQLVPVTLIAIVILAFV	660
Db	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQQKKGVIRESYLKGHDQLVPVTLIAIVILAFV	660
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKL SGLFGDTQSKDPKPE	720
Db	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKL SGLFGDTQSKDPKPE	720
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKREPSRGTREWERN	780
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ	840
Db	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ	840
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Qy	901	SKRLEMHHSSSYGV DYKRSYPTNSLTRSHQAT	932
Db	901	SKRLEMHHSSSYGV DYKRSYPTNSLTRSHLTT	932

RESULT 6

ADA23281

ID ADA23281 standard; protein; 939 AA.

XX

AC ADA23281;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide, SEC2.

XX
 KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
 KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
 KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
 KW cardiovascular disease; oncology disease; immune disorder;
 KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
 KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
 KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
 KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
 KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
 KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
 KW antiallergic; cardiant; dermatological.
 XX
 OS Homo sapiens.
 XX
 PN US2003054514-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 19-SEP-2001; 2001US-00957187.
 XX
 PR 09-MAR-1999; 99US-0123667P.
 PR 04-JAN-2000; 2000US-0174485P.
 PR 08-MAR-2000; 2000US-00520781.
 PR 19-SEP-2000; 2000US-0233798P.
 PR 20-SEP-2000; 2000US-0234082P.
 XX
 PA (SHIM/) SHIMKETS R A.
 PA (LARO/) LAROCHELLE W J.
 XX
 PI Shimkets RA, Larochelle WJ;
 XX
 DR WPI; 2003-540616/51.
 DR N-PSDB; ADA23280.
 XX
 PT New SECX nucleic acids, useful for treating or diagnosing a disorder
 PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
 PT and autoimmune disease.
 XX
 PS Claim 12; Fig 2; 118pp; English.
 XX
 CC The present invention relates to the isolation of human secreted or
 CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
 CC polynucleotide sequences encoding them. Also disclosed is a method for
 CC screening for a modulator of activity or latency of SECX. The SECX
 CC polypeptide and polynucleotide sequences may be used for treating or
 CC preventing SECX-associated disorders such as lung cancer, cardiovascular
 CC and oncology diseases, immune disorders, autoimmune diseases, transplant
 CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
 CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
 CC cord injuries, and skeletal disorders. The present sequence represents a
 CC SECX polypeptide of the invention.
 XX
 SQ Sequence 939 AA;

Query Match

90.3%; Score 4921; DB 6; Length 939;

Best Local Similarity 99.6%; Pred. No. 0;
Matches 928; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
      |||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120
      |||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120

Qy    121 IKVLLKKND DALFVCGTNAFNPNSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
      |||
Db    121 IKVLLKKND DALFVCGTNAFNPNSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
      |||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
      |||
Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPPER 360
      |||
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPPER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
      |||
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
      |||
Db    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480

Qy    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG 540
      |||
Db    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG 540

Qy    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600
      |||
Db    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600

Qy    601 GGMLDWKHL DSDPDST DPLGAVSSH NHQDKKGVIRESYLK GHDQLVPV TLLAIAVILAFV 660
      |||
Db    601 GGMLDWKHL DSDPDST DPLGAVSSH NHQDKKGVIRESYLK GHDQLVPV TLLAIAVILAFV 660

Qy    661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE 720
      |||
Db    661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE 720

Qy    721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSRREWERN 780
      |||
Db    721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKREPSRGRTREWERN 780

Qy    781 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ 840
      |||
```

Db 781 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ 840

Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
 |||

Db 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900

Qy 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQAT 932
 |||

Db 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHLTT 932

RESULT 7

AAB23031

ID AAB23031 standard; protein; 884 AA.

XX

AC AAB23031;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant, SECX 2864933-2.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
 KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200053742-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US006280.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR N-PSDB; AAA93618.

XX

PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of
 PT pathological states such as cancer, immune, cardiovascular and
 PT neurological disorders.

XX

PS Claim 1; Fig 3; 151pp; English.

XX

CC Sequences AAB23029-B23048 represent human SECX proteins. The SECX
 CC proteins of the invention are either secreted or membrane-associated
 CC proteins and act as regulator of cellular proliferation and
 CC differentiation. SECX proteins or nucleotides are useful for diagnosing
 CC the presence of, or predisposition to, a disease associated with altered
 CC levels of SECX proteins and nucleotides. The SECX proteins are also
 CC useful to screen compounds that modulate SECX activity or expression. The
 CC interaction of a SECX protein with other cellular proteins may be useful
 CC to modulate the activity of a partner protein, cellular proliferation,
 CC cellular differentiation and cell survival. SECX nucleotides are useful
 CC for the recombinant expression of SECX protein, and may be used detect
 CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to
 CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX
 CC nucleic acid sequences are also useful for identifying a cell or tissue
 CC type in a biological sample, and in forensic biology. SECX primers or
 CC probes are useful for detecting the presence of SECX nucleotides and for
 CC screening tissue cultures for contamination. Diseases that may be treated
 CC or prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
 CC or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 884 AA;

Query Match 84.2%; Score 4590.5; DB 3; Length 884;
 Best Local Similarity 93.7%; Pred. No. 0;
 Matches 873; Conservative 2; Mismatches 2; Indels 55; Gaps 1;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPI	ISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Db	1	MRSEALLLYFTLLHFAGAGFPEDSEPI	ISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTV	DIDTSHTEEIYCSKKLTWKS	RQADV
Db	61	IMIMNGTLYIAARDHIYTV	DIDTSHTEEIYCSKKLTWKS	RQADV
Qy	121	IKVLLKKNDALFVCGTNAFNP	SCRNYKMDTLEPFGDEFSGMARC	PYDAKHANVALFADG
Db	121	IKVLLKKNDALFVCGTNAFNP	SCRNYKMDTLEPFGDEFSGMARC	PYDAKHANVALFADG
Qy	181	KLYSATVTDFLAIDAVIYRSL	GESPTLRTVKHDSKWLKEPYFVQ	AVDYGDIYFFFREIA
Db	181	KLYSATVTDFLAIDAVIYRSL	GESPTLRTVKHDSKWLKEPYFVQ	AVDYGDIYFFFREIA
Qy	241	VEYNTMGKVVFPRVAQVCKND	MGGSQRVLEKQWTSFLKARLNCS	VPGDSHFYFNILQAVT
Db	241	VEYNTMGKVVFPRVAQVCKND	MGGSQRVLEKQWTSFLKARLNCS	VPGDSHFYFNILQAVT
Qy	301	DVIRINGRDVVLATFSTPYNS	IPGSAVCAYDMLDIASVFTGRFKEQKSPD	STWTPVPDER
Db	301	DVIRINGRDVVLATFSTPYNS	IPGSAVCAYDMLDIASVFTGRFKEQKSPD	STWTPVPDER
Qy	361	VPKPRPGCCAGSSSLERYATS	NEFPDDTLNFIKTHPLMDEAVPSIFNRPWFL	RTMVRRL

Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG	540
Db	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR	600
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	576
Qy	601	GGMLDWKHLSDSPDSTDPLGAVSSHNDKKGVIRESYLKGHDQLVPVTLLAIAVILAFV	660
Db	577	-----GVIRESYLKGHDQLVPVTLLAIAVILAFV	605
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	606	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	665
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
		: : :	
Db	666	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKREPSRGTRREWERN	725
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	840
Db	726	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	785
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	786	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	845
Qy	901	SKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQAT	932
Db	846	SKRLEMHHSSSYGVVDYKRSYPTNSLTRSHLTT	877

RESULT 8

ADA23283

ID ADA23283 standard; protein; 884 AA.

XX

AC ADA23283;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide, SEC3 #1.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;

KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;

KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;

KW cardiovascular disease; oncology disease; immune disorder;

KW autoimmune disease; transplant rejection; allergy; AIDS; infections;

KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;

KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;

KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

Db	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEFPFGDEFSGMARCPYDAKHANVALFADG	180
Db	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEFPFGDEFSGMARCPYDAKHANVALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Db	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRAVQCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRAVQCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG	540
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	576
Qy	601	GGMLDWKHL LDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGH DQLVPV TLLAIAVILAFV	660
Db	577	-----GVIRESYLKGH DQLVPV TLLAIAVILAFV	605
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	606	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	665
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	666	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKREPSRGTREWERN	725
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ	840
Db	726	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ	785
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	786	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	845
Qy	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQAT	932
Db	846	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHLT	877

RESULT 9

AAB95139

ID AAB95139 standard; protein; 699 AA.

XX

AC AAB95139;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:17154.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX

PS Claim 8; SEQ ID NO 17154; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX

SQ Sequence 699 AA;

Query Match 67.5%; Score 3677; DB 4; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.2e-307;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      332 MLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF 391
          |||
Db       1 MLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF 60

Qy      392 IKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVFLGSEKGIILKFL 451
          |||
Db       61 IKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVFLGSEKGIILKFL 120

Qy      452 ARIGNSGFLNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP 511
          |||
Db      121 ARIGNSGFLNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP 180

Qy      512 LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS 571
          |||
Db      181 LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS 240

Qy      572 FVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSH NHQDKK 631
          |||
Db      241 FVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSH NHQDKK 300

Qy      632 GVIRESYLK GHDQLVPVTL LAIAVILAFVMGAVFSGITVYCVCDHRRKDVA VVQRKEKEL 691
          |||
Db      301 GVIRESYLK GHDQLVPVTL LAIAVILAFVMGAVFSGITVYCVCDHRRKDVA VVQRKEKEL 360

Qy      692 THSR RGSMS SVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQH HLD 751
          |||
Db      361 THSR RGSMS SVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQH HLD 420

Qy      752 LTALPTPESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGSPVIPTDLPLRASPSH 811
          |||
Db      421 LTALPTPESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGSPVIPTDLPLRASPSH 480

Qy      812 IPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV 871
          |||
Db      481 IPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV 540

Qy      872 ENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA 931
          |||
Db      541 ENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA 600

Qy      932 TTLKRNTN SSNSSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNA 991
          |||
Db      601 TTLKRNTN SSNSSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNA 660
```

QY 992 YNSLTRSGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT 1030
|||||
Db 661 YNSLTRSGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT 699

RESULT 10

AAB23043

ID AAB23043 standard; protein; 630 AA.

XX

AC AAB23043;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant, SECX pCR2.1-2864933.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200053742-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US006280.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR N-PSDB; AAA93630.

XX

PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.

XX

PS Claim 1; Fig 15; 151pp; English.

XX

CC Sequences AAB23029-B23048 represent human SECX proteins. The SECX
CC proteins of the invention are either secreted or membrane-associated
CC proteins and act as regulator of cellular proliferation and
CC differentiation. SECX proteins or nucleotides are useful for diagnosing
CC the presence of, or predisposition to, a disease associated with altered

CC levels of SECX proteins and nucleotides. The SECX proteins are also
 CC useful to screen compounds that modulate SECX activity or expression. The
 CC interaction of a SECX protein with other cellular proteins may be useful
 CC to modulate the activity of a partner protein, cellular proliferation,
 CC cellular differentiation and cell survival. SECX nucleotides are useful
 CC for the recombinant expression of SECX protein, and may be used detect
 CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to
 CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX
 CC nucleic acid sequences are also useful for identifying a cell or tissue
 CC type in a biological sample, and in forensic biology. SECX primers or
 CC probes are useful for detecting the presence of SECX nucleotides and for
 CC screening tissue cultures for contamination. Diseases that may be treated
 CC or prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
 CC or traumatic wounds, spinal cord injury), and skeletal disorders
 XX
 SQ Sequence 630 AA;

Query Match 61.9%; Score 3373; DB 3; Length 630;
 Best Local Similarity 99.8%; Pred. No. 1.8e-281;
 Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	17	GAGFPEDSEPI	SHGNYTKQYPVFVGHK	PGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	76
		:			
Db	1	GSGFPEDSEPI	SHGNYTKQYPVFVGHK	PGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	60
Qy	77	YTVDIDTSHTEEIYCSK	KLTKWSRQADVDTCRMKGKHKDECHNFIKVL	LKKND DALFVCG	136
Db	61	YTVDIDTSHTEEIYCSK	KLTKWSRQADVDTCRMKGKHKDECHNFIKVL	LKKND DALFVCG	120
Qy	137	TNAFNPSCRNYKMDTLE	PFSGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV	196	
Db	121	TNAFNPSCRNYKMDTLE	PFSGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV	180	
Qy	197	IYRSLGESPTLRTVKH	DSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFP	PRVAQ	256
Db	181	IYRSLGESPTLRTVKH	DSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFP	PRVAQ	240
Qy	257	VCKNDMGGSQRVLEKQ	WTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS	316	
Db	241	VCKNDMGGSQRVLEKQ	WTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS	300	
Qy	317	TPYNSIPGSAVCAYDML	DIASVFTGRFKEQKSPDSTWTFVPDERVPKPRPGCCAGSSSLE	376	
Db	301	TPYNSIPGSAVCAYDML	DIASVFTGRFKEQKSPDSTWTFVPDERVPKPRPGCCAGSSSLE	360	
Qy	377	RYATSNEFPDDTLNFI	KTHPLMDEAVPSIFNRPWFRLTMVRYRLTKIAVDTAAGPYQNHT	436	
Db	361	RYATSNEFPDDTLNFI	KTHPLMDEAVPSIFNRPWFRLTMVRYRLTKIAVDTAAGPYQNHT	420	
Qy	437	VVFLGSEKGIILKFLA	RIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	496	
Db	421	VVFLGSEKGIILKFLA	RIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	480	

QY 497 SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGGACSHLSPNSRLTFEQD 556
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGGACSHLSPNSRLTFEQD 540
 QY 557 IERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDST 616
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 IERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDST 600
 QY 617 DPLGAVSSHNHQDKKGVIRESYLKGHQDL 645
 ||||||||||||||||||||||||||||
 Db 601 DPLGAVSSHNHQDKKGVIRESYLKGHQDL 629

RESULT 11

ADA23307

ID ADA23307 standard; protein; 630 AA.

XX

AC ADA23307;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;

KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;

KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;

KW cardiovascular disease; oncology disease; immune disorder;

KW autoimmune disease; transplant rejection; allergy; AIDS; infections;

KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;

KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;

KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;

KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;

KW antiallergic; cardiant; dermatological.

XX

OS Homo sapiens.

XX

PN US2003054514-A1.

XX

PD 20-MAR-2003.

XX

PF 19-SEP-2001; 2001US-00957187.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 04-JAN-2000; 2000US-0174485P.

PR 08-MAR-2000; 2000US-00520781.

PR 19-SEP-2000; 2000US-0233798P.

PR 20-SEP-2000; 2000US-0234082P.

XX

PA (SHIM/) SHIMKETS R A.

PA (LARO/) LAROCHELLE W J.

XX

PI Shimkets RA, Larochelle WJ;

XX

DR WPI; 2003-540616/51.

DR N-PSDB; ADA23306.

XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.

XX
PS Claim 12; Fig 15; 118pp; English.

XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence represents a
CC SECX polypeptide of the invention.

XX
SQ Sequence 630 AA;

Query Match 61.9%; Score 3373; DB 6; Length 630;
Best Local Similarity 99.8%; Pred. No. 1.8e-281;
Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 17 GAGFPEDSEPI SISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI 76
|:|||||||||||||||||||||||||||||||||||||||||
Db 1 GSGFPEDSEPI SISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI 60

Qy 77 YTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNFIKVLKKNDDALFVCG 136
|||||||||||||||||||||||||||||||||||||||||
Db 61 YTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNFIKVLKKNDDALFVCG 120

Qy 137 TNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV 196
|||||||||||||||||||||||||||||||||||||||||
Db 121 TNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV 180

Qy 197 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ 256
|||||||||||||||||||||||||||||||||||||||||
Db 181 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ 240

Qy 257 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 316
|||||||||||||||||||||||||||||||||||||||||
Db 241 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 300

Qy 317 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE 376
|||||||||||||||||||||||||||||||||||||||||
Db 301 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE 360

Qy 377 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT 436
|||||||||||||||||||||||||||||||||||||||||
Db 361 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT 420

Qy 437 VVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS 496
|||||||||||||||||||||||||||||||||||||||||
Db 421 VVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS 480

Qy 497 SSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD 556
 |||
 Db 481 SSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD 540
 Qy 557 IERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLDSPDST 616
 |||
 Db 541 IERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLDSPDST 600
 Qy 617 DPLGAVSSHNHQDKKGVIRESYLKGHQDL 645
 |||
 Db 601 DPLGAVSSHNHQDKKGVIRESYLKGHQDL 629

RESULT 12

ADA23360

ID ADA23360 standard; protein; 626 AA.

XX

AC ADA23360;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide, SEC3 #2.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;

KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;

KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;

KW cardiovascular disease; oncology disease; immune disorder;

KW autoimmune disease; transplant rejection; allergy; AIDS; infections;

KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;

KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;

KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;

KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;

KW antiallergic; cardiant; dermatological.

XX

OS Homo sapiens.

XX

PN US2003054514-A1.

XX

PD 20-MAR-2003.

XX

PF 19-SEP-2001; 2001US-00957187.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 04-JAN-2000; 2000US-0174485P.

PR 08-MAR-2000; 2000US-00520781.

PR 19-SEP-2000; 2000US-0233798P.

PR 20-SEP-2000; 2000US-0234082P.

XX

PA (SHIM/) SHIMKETS R A.

PA (LARO/) LAROCHELLE W J.

XX

PI Shimkets RA, Larochelle WJ;

XX

DR WPI; 2003-540616/51.

DR N-PSDB; ADA23359.

XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 12; Page 7; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence represents a
CC SECX polypeptide of the invention.
XX
SQ Sequence 626 AA;

Query Match 61.7%; Score 3362; DB 6; Length 626;
Best Local Similarity 100.0%; Pred. No. 1.6e-280;
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	19	GFPEDSEPI	SHGNYTKQYPVFVGHK	PGRNTTQRHRLDIQMIMIMNGTLYIAARDHIYT	78
Db	1	GFPEDSEPI	SHGNYTKQYPVFVGHK	PGRNTTQRHRLDIQMIMIMNGTLYIAARDHIYT	60
Qy	79	VDIDTSHTEEIYCSK	KLTKWSRQADV	TCRMKGKHKDECHNFIKVL	138
Db	61	VDIDTSHTEEIYCSK	KLTKWSRQADV	TCRMKGKHKDECHNFIKVL	120
Qy	139	AFNPSCRNYKMDTLE	PFPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAVIY	198	
Db	121	AFNPSCRNYKMDTLE	PFPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAVIY	180	
Qy	199	RSLGESPTLRTVKH	DSKWLKEPYFVQAVDYGDYIYFFFREIAVEYNTMGKVVFP	258	
Db	181	RSLGESPTLRTVKH	DSKWLKEPYFVQAVDYGDYIYFFFREIAVEYNTMGKVVFP	240	
Qy	259	KNDMGGSQRVLEKQ	WTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFSTP	318	
Db	241	KNDMGGSQRVLEKQ	WTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFSTP	300	
Qy	319	YNSIPGSAVCAYDML	DIASVFTGRFKEQKSPDSTWTPVDPDERVPKPRPGCCAGSSSLERY	378	
Db	301	YNSIPGSAVCAYDML	DIASVFTGRFKEQKSPDSTWTPVDPDERVPKPRPGCCAGSSSLERY	360	
Qy	379	ATSNEFPDDTLNFI	KTHPLMDEAVPSIFNRPWFLRTMVRRLTKIAVDTAAGPYQNHTTV	438	
Db	361	ATSNEFPDDTLNFI	KTHPLMDEAVPSIFNRPWFLRTMVRRLTKIAVDTAAGPYQNHTTV	420	
Qy	439	FLGSEKGIILKFLA	RIGNSGFLNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSS	498	
Db	421	FLGSEKGIILKFLA	RIGNSGFLNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSS	480	

QY 499 LYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIE 558
 |||
 Db 481 LYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIE 540
 QY 559 RGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDP 618
 |||
 Db 541 RGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDP 600
 QY 619 LGAVSSHNHQDKKGVIRESYLKGHQDQ 644
 |||
 Db 601 LGAVSSHNHQDKKGVIRESYLKGHQDQ 626

RESULT 13

AAB95317

ID AAB95317 standard; protein; 574 AA.

XX

AC AAB95317;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:17568.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.

XX

PS Claim 8; SEQ ID NO 17568; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 574 AA;

Query Match 54.7%; Score 2980.5; DB 4; Length 574;
 Best Local Similarity 90.7%; Pred. No. 1.2e-247;
 Matches 574; Conservative 0; Mismatches 0; Indels 59; Gaps 1;

Qy	398	MDEAVPSIFNRPWFLRTMVR	YRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNS	457
Db	1	MDEAVPSIFNRPWFLRTMVR		20
Qy	458	GFLNDSLFLLEEMSVYNSEKCSYDGV	EDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR	517
Db	21	-----CSYDGV	EDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR	61
Qy	518	HGCKKKTCIASRDPYCGWIK	EGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG	577
Db	62	HGCKKKTCIASRDPYCGWIK	EGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG	121
Qy	578	HSSSLLPSTTTSDSTAQEGYESR	GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGV	637
Db	122	HSSSLLPSTTTSDSTAQEGYESR	GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGV	181
Qy	638	YLGHDQLVPVTLIAIVILAFVMG	AVFSGITVYCVCDHRRKDVAVVQRKEKELTHSR	697
Db	182	YLGHDQLVPVTLIAIVILAFVMG	AVFSGITVYCVCDHRRKDVAVVQRKEKELTHSR	241
Qy	698	SMSSVTKL	SGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPT	757
Db	242	SMSSVTKL	SGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPT	301
Qy	758	PESTPTLQQKRKPSRGSREWERNQ	NLINACTKDMPPMGSPVIPTDLPLRASPSHIP	817
Db	302	PESTPTLQQKRKPSRGSREWERNQ	NLINACTKDMPPMGSPVIPTDLPLRASPSHIP	361
Qy	818	LPITQQGYQHEYVDQPKMSEVAQ	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL	877
Db	362	LPITQQGYQHEYVDQPKMSEVAQ	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL	421

Qy 878 PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRN 937
 |||
 Db 422 PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRN 481
 Qy 938 NTNSSNSSHLNRNQSFGRGDNPPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR 997
 |||
 Db 482 NTNSSNSSHLNRNQSFGRGDNPPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR 541
 Qy 998 SGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT 1030
 |||
 Db 542 SGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT 574

RESULT 14

AAB94104

ID AAB94104 standard; protein; 562 AA.

XX

AC AAB94104;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:14328.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-

PT length cDNAs defined in the specification, and for the detection and/or

PT diagnosis of the abnormality of the proteins encoded by the full-length

PT cDNAs.

XX

PS Claim 8; SEQ ID NO 14328; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-

CC length cDNAs defined in the specification. Where a primer set comprises:

CC (a) an oligo-dT primer and an oligonucleotide complementary to the

Qy 949 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 1008
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 540
 Qy 1009 DVPPKPSFAPLSTSMKPNDACT 1030
 ||||||||||||||||
 Db 541 DVPPKPSFAPLSTSMKPNDACT 562

RESULT 15

AAM93444

ID AAM93444 standard; protein; 562 AA.

XX

AC AAM93444;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 3088.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-00114089.

XX

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

DR WPI; 2001-524255/58.

DR N-PSDB; AAK94365.

XX

PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.

XX

PS Claim 8; SEQ ID NO 3088; 1380pp + Sequence Listing; English.

XX

CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesising the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 562 AA;

Query Match 54.1%; Score 2947; DB 4; Length 562;
Best Local Similarity 99.8%; Pred. No. 8.7e-245;
Matches 561; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYAFSTCVIKVPLGRRCERHGKCKKTCIAS 528
          |||
Db       1 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYAFSTCVIKVPLGRRCERHGKCKKTCIAS 60

Qy      529 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT 588
          |||
Db       61 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT 120

Qy      589 SDSTAQEGYESRGGMLDWKHLSDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQVPV 648
          |||
Db      121 SDSTAQEGYESRGGMLDWKHLSDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQVPV 180

Qy      649 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGL 708
          |||
Db      181 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGL 240

Qy      709 FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKR 768
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Db      241 FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKR 300

Qy      769 KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE 828
          |||
Db      301 KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE 360

Qy      829 YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL 888
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Db      361 YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL 420

Qy      889 GPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLS 948
          |||
Db      421 GPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLS 480

Qy      949 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 1008
          |||
Db      481 RNQSFGRGDSPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 540

Qy     1009 DVPPKPSFAPLSTSMKPNDACT 1030
          |||
Db      541 DVPPKPSFAPLSTSMKPNDACT 562
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Search completed: March 24, 2004, 13:14:21
Job time : 104.009 secs

OM protein - protein search, using sw model

Run on: March 24, 2004, 13:12:28 ; Search time 32.7132 Seconds
(without alignments)
1625.481 Million cell updates/sec

Title: US-09-856-681A-2
Perfect score: 5450
Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

8							
Result	Query					Description	
No.	Score	Match	Length	DB	ID		
1	2361.5	43.3	1086	4	US-09-653-274-4	Sequence 4, Appli	
2	2354	43.2	1070	4	US-09-653-274-8	Sequence 8, Appli	
3	2013.5	36.9	888	4	US-09-077-940A-4	Sequence 4, Appli	
4	1997	36.6	887	4	US-09-077-940A-2	Sequence 2, Appli	
5	1923	35.3	641	4	US-09-653-274-13	Sequence 13, Appl	
6	1519.5	27.9	930	4	US-09-254-594-6	Sequence 6, Appli	
7	1428.5	26.2	929	4	US-09-254-594-3	Sequence 3, Appli	
8	1377.5	25.3	536	4	US-09-653-274-10	Sequence 10, Appl	
9	969.5	17.8	730	1	US-08-121-713D-58	Sequence 58, Appl	
10	969.5	17.8	730	1	US-08-835-268-58	Sequence 58, Appl	
11	969.5	17.8	730	2	US-09-060-692-58	Sequence 58, Appl	

12	969.5	17.8	730	3	US-08-833-391-58	Sequence 58, Appl
13	969.5	17.8	730	4	US-09-060-610-58	Sequence 58, Appl
14	969.5	17.8	730	5	PCT-US94-10151A-58	Sequence 58, Appl
15	880	16.1	650	1	US-08-121-713D-60	Sequence 60, Appl
16	880	16.1	650	1	US-08-835-268-60	Sequence 60, Appl
17	880	16.1	650	2	US-09-060-692-60	Sequence 60, Appl
18	880	16.1	650	3	US-08-833-391-60	Sequence 60, Appl
19	880	16.1	650	4	US-09-060-610-60	Sequence 60, Appl
20	880	16.1	650	5	PCT-US94-10151A-60	Sequence 60, Appl
21	852.5	15.6	655	4	US-08-556-422A-3	Sequence 3, Appli
22	852.5	15.6	771	1	US-08-121-713D-54	Sequence 54, Appl
23	852.5	15.6	771	1	US-08-835-268-54	Sequence 54, Appl
24	852.5	15.6	771	2	US-09-060-692-54	Sequence 54, Appl
25	852.5	15.6	771	3	US-08-833-391-54	Sequence 54, Appl
26	852.5	15.6	771	4	US-09-060-610-54	Sequence 54, Appl
27	852.5	15.6	771	5	PCT-US94-10151A-54	Sequence 54, Appl
28	845	15.5	712	1	US-08-121-713D-64	Sequence 64, Appl
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30	845	15.5	712	2	US-09-060-692-64	Sequence 64, Appl
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32	845	15.5	712	4	US-09-060-610-64	Sequence 64, Appl
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34	779.5	14.3	724	1	US-08-121-713D-62	Sequence 62, Appl
35	779.5	14.3	724	1	US-08-835-268-62	Sequence 62, Appl
36	779.5	14.3	724	2	US-09-060-692-62	Sequence 62, Appl
37	779.5	14.3	724	3	US-08-833-391-62	Sequence 62, Appl
38	779.5	14.3	724	4	US-09-060-610-62	Sequence 62, Appl
39	779.5	14.3	724	5	PCT-US94-10151A-62	Sequence 62, Appl
40	748	13.7	775	4	US-09-308-179B-1	Sequence 1, Appli
41	736.5	13.5	862	4	US-08-556-422A-2	Sequence 2, Appli
42	654.5	12.0	607	4	US-08-556-422A-4	Sequence 4, Appli
43	586	10.8	477	1	US-08-136-922-2	Sequence 2, Appli
44	539	9.9	425	4	US-08-556-422A-7	Sequence 7, Appli
45	462	8.5	295	4	US-08-556-422A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-653-274-4

; Sequence 4, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

Qy	611	--DSP---DSTDPLGAVSSSHNHQDKKGVIRESYLKGHDQLVPVPTLLAIAVILAFVMGAVF	665
Db	639	VQDDPNTSDFTDPLSGI-----PKGVRWEVQSGESNQMVHMVNLITCVFAAFVLGAFT	691
Qy	666	SGITVYCVCD-HRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFG----DTQSKDPKPE	720
Db	692	AGVAVYCYRDMFVRKNRKI--HKDAESAQSCDTSSGSFAKLNGLFDSFVKEYQQNIDSPK	749
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	750	LYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPTPESTPVLHQKTLQAMKSHSEKAH	809
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEY-----	829
Db	810	GH--GASRKETPQFFPSSPPPHSPL--SHGHIPSAIVLPNATHDYNTSFSNSNAHKAEEK	865
Qy	830	---VDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPN-----HGVNLVE	872
Db	866	LQNIDHPLTKSSSKRDHRRSVDSRNTL--NDLLKHLNDPNSNPKAIMGDIQMAHQNLMLD	923
Qy	873	NLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSY---GVDYKRSYPTNSLT	926
Db	924	PMGSMSEVPPKPVNREASLYSPSTLPRNSPTKRVDVPTTPGVPMTSLERQRGYHKNSSQ	983
Qy	927	RSHQATTLKRNNNTSSNSSHLSRNQSFGRGD-NPPPPAPQRVDSIQVHSSQPSGQAVTVSR	985
Db	984	R-HSISAMPK-NLNSPNGVLLSRQPSMNRGGYMPFTGTAKVDYIQ-----GTPVSVHL	1034
Qy	986	QPSLNAYNSLT-----RSGLKRTPSLKPDVPPKPSFAPLSTSMKP	1025
Db	1035	QPSLSRQSSYTSNGTLPRGTGLKRTPSLKPDVPPKPSFVPQTPSVRP	1080

RESULT 2

US-09-653-274-8

; Sequence 8, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

10 TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-10

; NUMBER OF SEO ID NOS: 13

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; SOFTWARE: PatentIn Ver. 2.1

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; SEO ID NO 8

LENGTH: 1070

; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-653-274-8

Query Match 43.2%; Score 2354; DB 4; Length 1070;
Best Local Similarity 45.8%; Pred. No. 1.1e-214;
Matches 506; Conservative 159; Mismatches 295; Indels 144; Gaps 29;

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Qy      20 FPEDESEPISSHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMMNGTLYIAARDHIYTV 79
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Db      7 FPEDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLDFQLMLKIRDTLYIAGRDQVYTV 64

Qy     80 DIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKNDALFVCGTNA 139
      ::: | : ||||:|| | : | ||||| ||||| : ||: : |||||
Db     65 NLNEMPKEVIPNKKLTWRSRQQDRENCAMKGKHKDECHNFIKVFPVRNDEMVFVCGTNA 124

Qy    140 FNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAVIYR 199
      ||| || |:: || | :| ||:||||:|: | ||||| ||||| |||| | ||||
Db    125 FNPMSCRYRLSTLEYDGEEISGLARCPFDARQTNVALFADGKLYSATVADFLASDAVIYR 184

Qy    200 SLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQVCK 259
      |::: |||:|:||||:||||: |:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    185 SMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYVFFFREIAVEHNNLGKAVYSRVARICK 244

Qy    260 NDMGGSQRVLEKQWTSFLKARLNCVPGDSHFYFNILQAVTDVIRINGRDVVLATFSTPY 319
      ||||| ||||| ||||| ||||| ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    245 NDMGGSQRVLEKHWTSFLKARLNCVPGDPFFYFDVLSITDIIQINGIPTVVGVTTLQL 304

Qy    320 NSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVVPKPRPGCCAGSSSLERYA 379
      ||||| ||||:| || || |||||:| || ||:|:| ||||| || || ||
Db    305 NSIPGSAVCAFSMDIEKVFKGRFKEQKTPDSVWTAVPEDKVPKPRPGCCAKHGLAEAYK 364

Qy    380 TSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYLRTKIAVDTAAGPYQNHTVVF 439
      || :||:|:|:|:|:| || | : || :| |||| |:| | :|||:|:|:|
Db    365 TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFTKTRVRYRLTAISVDHSAGPYQNYTVIF 424

Qy    440 LGSEKGIILKFLARIGNSGF-LNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSS 498
      :||| |::|| ||: | | ||||: ||: || || : |||::: :||: :
Db    425 VGSEAGMVLKVLAK--TSPFSLNDSVLLLEEIEAYNHAKCSAENEEDKKVISLQLDKDHHA 482

Qy    499 LYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLT----- 552
      |||||:|:|:|:| ||||:| |||:|||||||:|:|:|:|:|:|:|:|
Db    483 LYVAFSSCIIRIPLSRCERYGCKKSCIASRDPYCGWLSQ-GSCGRVTPGMLLLTEDFFA 541

Qy    553 -----FEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGG-- 602
      :||| | || | |||| :||:| || | : ||
Db    542 FHNHSAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD-----YKIFGGPT 584

Qy    603 -----MLD-WKHLL-----DSP---DSTDPLGAVSSSHNH 627
      :|| | : | | | | |||| :
Db    585 SDMEVSSSSVTTMASIPEITPKVIDTWRPKLTSSRKFFVQDDPNTSDFTDPLSGI----- 639

Qy    628 QDKKGVIRESYLKGHDQLVPVTLIAIVILAFVMGAVFSGITVYCVCD-HRRKDVAVVQR 686
      ||| | :||:|:| | |||:| |:| || | ||:|
Db    640 --PKGVRWEVQSGESNQMVHMNVLITCVFAAFVLGAFIAGVAVYCYRDMFVRKRNKI--H 695

Qy    687 KEKELTHSRRGSMSSVTKLSGLFG----DTQSKDPKPEAILTPLMHNGKLATPGNTAKML 742
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Db      696 KDAESAQSCTDSSSGSFAKLNGLFDSPVKEYQQNIDSPKLYSNLLTSRKELPPNGDTKSMV 755
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      :      :| ||||| || | | : | : : : | |: | |
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Qy      803 LPLRASPSHIPSVVVLPIITQQGYQHEY-----VDQP---KMSEVAQMALED 845
      || | | ||| :|| | : : | | | : |
Db      814 SPL--SHGHIPSAIVLPNATHDYNTSFSNSNAHKAEEKLQNIHPLTKSSSKRDHRRSVD 871
Qy      846 QAATLEYKTIKEHLSSKSPN-----HGVNLVENLDSL---PPKVPQREASLGPP 891
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Db      872 SRNTL--NDLLKHLNDPNSNPKAIMGDIQMAHQNLMLDPMGSMSEVPKVPNREASLYSP 929
Qy      892 GASLSQTGLSKRLEMHHSSSY---GVDYKRSYPTNSLTRSHQATTLKRNTNTSSNSSHLS 948
      ::| : :||:: : : : :| | | | : : : | | | ||
Db      930 PSTLPRNSPTKRVDVPTTPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NLNSPNGVLLS 987
Qy      949 RNQSFGRGD-NPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSLGK 1001
      | | || | | :|| || | |:| |||: :| | | :|||
Db      988 RQPSMNRGGYMPPTPTGAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSNGTLPRTGLK 1040
Qy      1002 RTPSLKPDVPPKPSFAPLSTSMKP 1025
      ||||| ||||| || | : |::|
Db      1041 RTPSLKPDVPPKPSFVPQTPSVRP 1064

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RESULT 3

US-09-077-940A-4

; Sequence 4, Application US/09077940A

; Patent No. 6576441

; GENERAL INFORMATION:

; APPLICANT: KIMURA, Toru et al.

; TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME

; FILE REFERENCE: 0020-4426P

; CURRENT APPLICATION NUMBER: US/09/077,940A

; CURRENT FILING DATE: 1998-06-05

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 888

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-077-940A-4

Query Match 36.9%; Score 2013.5; DB 4; Length 888;

Best Local Similarity 45.3%; Pred. No. 2.3e-182;

Matches 424; Conservative 129; Mismatches 241; Indels 141; Gaps 20;

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Db      12 ALLLLLLLLGGAGHLFPEDPPPLSVAPRDYLNHYVPFVSGPGRLTPAEGADDLNIQRVL 71
Qy      63 IMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNFIK 122
      :| ||:| ||::| |:: :| :|||:| :|:: |||| : || ||:|
Db      72 RVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGECRNFKV 131

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Qy 123 VLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKL 182
 ||| ::| | | | : | | | | | | | | : | | | | | | | | | | : | | |
 Db 132 VLLLRDESTLFVCGSNAFN PVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDGML 191

Qy 183 YSATVTDFLAIDAVIYRSLGESPTLRITVKHDSKWLKEPYFVQAVDYGDIYFFFR EIAVE 242
 ::| | | | | | | | | | | | | | : | | | | | | | | | | | | | | : | | | | | | | | : |
 Db 192 FTATVTDFLAIDAVIYRSLGDRPTLRITVKHDSKWFKEPYFVH AVEW GSHVYFFFR EIAVE 251

Qy 243 YNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDV 302
 : | : | | | | | | : | | | | | | : | | | | | | | | | | | | | | : | | | | |
 Db 252 FNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTGV 311

Qy 303 IRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVP 362
 : : | | | | | | | | | | | | | | : : | | | | | | : | | | | | : : | |
 Db 312 VSLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVA AVFEGRFREQKSPESIWTPVPEDQVP 371

Qy 363 KPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTK 422
 : | | | | | | : | | : | | | | | : | | | | | | : : | | | | : : | | :
 Db 372 RPRPGCCAAPGM--QYNASSALPDDILNFVKTHPLMDEAVPSLGHPWILRTLMRHQLTR 429

Qy 423 IAVDTAAGPYQNHTVVFLGSEKGIILKFLAR--IGNSGFLNDSL FLEEMSVYNSEKCSYD 480
 : | | | | | : | | | | | | | : | | | | | | | | | | : | | | | : |
 Db 430 VAVDVGAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRP 489

Qy 481 GVED--KRIMGMLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKE 538
 | : : | : : : | | | | | | | | | | : | : | : | | | | : | | | | :
 Db 490 GGGETGQRLLSLELDAASGGLLA AFPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPD 549

Qy 539 GGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYE 598
 | : | | | : | | | : | | | : | | | |
 Db 550 -GSCIFLSPGTRAAFEQDVSGASTSGLGDC----- 578

Qy 599 SRGGM LDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESYLK GHDQLVPVTL LAIAVILA 658
 | : : | | : | | | | | : : |
 Db 579 -----TGLLRASLSED RAGLVS VNLLVTSSVAA 606

Qy 659 FVMGAVFSGITV-YCVC DHRRKDVAVVQRKEKE--LTHSRRGSMSSVTKLSGLFGDTQSK 715
 | | : | | | | | : | : | | : | | : | | : | | : | | : | : :
 Db 607 FVVGAVVSGFSVGW FVGLRERRELA--RRKDKEAILAHGAGEAVLSVSRL----GERRAQ 660

Qy 716 DP-----KPEAILTPLMHNGKLATPGNTAK-MLIKADQHHLDTALPTPEST 761
 | | | | | | | | : | | | | | | | : | | | | | | | | | |
 Db 661 GPGGRGGGGGGGAGVPPEALLAPLMQNG-----WAKATLLQGGPHDLD SGLLP TPEQT 713

Qy 762 PTLQQKRKP-----SRGSREWERNQNLINACTKDMPPMGSPVIPTDLP---LRASPSH 811
 | | | | | | : | | | : | | : | | : | : | : | :
 Db 714 P-LPQKRLPTPHPHPALGPRAWDH-----GHPLL PASASSS LLLLAPAR 757

Qy 812 IPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV 871
 | | | | | : | : | | : : : : : : : : : :
 Db 758 APEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRRV-----SAPTGPLDPA 811

Qy 872 ENLDSL P-PKVPQREASL-----GPPGASLSQT 898
 | | | | | | | | | | : | : | : | : | : | :
 Db 812 SAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRT 846

RESULT 4

US-09-077-940A-2

; Sequence 2, Application US/09077940A

; Patent No. 6576441

; GENERAL INFORMATION:

; APPLICANT: KIMURA, Toru et al.

; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME

; FILE REFERENCE: 0020-4426P

; CURRENT APPLICATION NUMBER: US/09/077,940A

; CURRENT FILING DATE: 1998-06-05

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 887

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-09-077-940A-2

Query Match 36.6%; Score 1997; DB 4; Length 887;
Best Local Similarity 42.7%; Pred. No. 8.7e-181;
Matches 433; Conservative 132; Mismatches 260; Indels 190; Gaps 25;

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Qy      2 RSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQR--HRLDIQ 59
      |  | |  ||      ||:: ||:: :|  ||||  || |  |::|
Db      10 RPALLFLLLLLLRVTHGLFPDEPPPLSVAPRDYLSHYPVFVGSGPGRLTPAEGAEDLNIQ 69

Qy      60 MIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN 119
      :: :| ||:| ||::| |::| | : | : :|||:| :|:| ||||| : || |
Db      70 RVLRVNRTLFIGDRDNLYQVELEPSTSTELRYQRKLTWRSNPSDIDVCRMKGQEGECRN 129

Qy     120 FIKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFAD 179
      |:||| ::| |||:|||| | || |||: || ||||| |||||:|
Db     130 FVKVLLLRDESTLFVCGSNAFNPICANYSMDTLQLLGDNISGMARCPYDPKHANVALFSD 189

Qy     180 GKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREI 239
      | |::||||| |||||: ||||| ||||| ||||| ||::| ::|||
Db     190 GMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSVYFFFREI 249

Qy     240 AVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAV 299
      |:|:| : || | |::|||:| | ||||| ||||| |||||:|
Db     250 AMEFNYLEKVVSRRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAV 309

Qy     300 TDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDE 359
      | | : || |:| ||| ||||| |||||:| | :| | ||:| |||:|
Db     310 TGVVSLGGRPVILAVFSTPSNSIPGSAVCAFDMNQVAAVFEGRFREQKSPESIWTVPED 369

Qy     360 RVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYR 419
      :||:||||| :| || ||: ||:||||| |||: : || :|::|:
Db     370 QVPRPRPGCCAAPGM--QYNASNALPDEILNFVKTHPLMDEAVPSLGHSPWIVRTLIRHQ 427

Qy     420 LTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLAR--IGNSGFLNDSLFLEEMSVYNSEKC 477
      ||::|| | ||: | |:|||| | :||| : || | :||| | :|
Db     428 LTRVAVDVGAGPWGNQTIIVFLGSEVGTVLKFLVKPNASVSGTTGPSIFLEEFETYRPDRC 487

Qy     478 ---SYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCG 534
      | | :|:: :|| || | || ||::||: ||: : | | | |:|
Db     488 GRSSSAGEWGQRLLSLELDAASGGLLAAPRCVVRVPVARCQLYSGCMKNCIGSQDPYCG 547
```

Qy 535 WKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQ 594
 | : |:| | | : ||||: :| ||||
 Db 548 WAPD-GSCIFLRPGTSATFEQDVSGASTSGLGDC----- 580
 Qy 595 EGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLKQHDQLVPVTLAIA 654
 |::| | | | | | :
 Db 581 -----TGLLRASLSDDRAGLVSVNLLVTS 604
 Qy 655 VILAFVMGAVFSGITV-YCVCCHRRKDVAVVQRKEKE--LTHSRGSMSSVTKL----- 705
 : |||:|||| | :| : | |::| :||:| | | :| :| :|
 Db 605 SVAAFVVGAVVSGFVGVFWFGLRERRELA--RRKDKEAILAHGGSEAVLSVSRLGERRGT 662
 Qy 706 --SGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT 763
 | | | | | | | | | | | | : | | | | | | | |
 Db 663 GTGGRGGAGGGPGGPPEALLAPLMQNGW-----TKAALLHGGPHDLDLGLLPTPEQTP- 715
 Qy 764 LQQRKPSR-----GSREWERNQNLINACTK-----DMPPMGSPVIPTD-- 802
 | | | | : | | | : : |::| : | | :||:
 Db 716 LPQKRLPTTHPHAHALGPRAWDHSHALLSASASTSLLLLAHTRAPEQPP-----VPTESG 770
 Qy 803 -----LPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK 856
 | | | : | | | : : | : :
 Db 771 PESRLCAPRSCRASHPGDFPLTP-----HASPDRRRVVSAPTGPLDSSSVG----- 816
 Qy 857 EHLSSKSPNHGVNLVENLDSLP-PKVPQREASL-----GPPGASLSQTGLSKRLEMHHS 909
 | | | | | :|| | | | :| :| :|
 Db 817 -----DDLPGPWSPPATSSLRPGPHGPPTAALRRT-----HT 849
 Qy 910 SSYGVYDKRSYPTNSLTRSHQATTLLKRNNTNSSNSSHLSRNQSFGRGD-NPPPPAP 963
 : | : | | | :||:| | | : | | |
 Db 850 FNSG----EARPGGHRPRRHA-----PADSTHL---LPCGTGERTAPPVP 887

RESULT 5

US-09-653-274-13

; Sequence 13, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 641

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-653-274-13

Query Match 35.3%; Score 1923; DB 4; Length 641;
Best Local Similarity 55.3%; Pred. No. 5.5e-174;
Matches 362; Conservative 101; Mismatches 118; Indels 74; Gaps 12;

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Qy      20  FPEDESEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMMNGTLYIAARDHIYTV 79
      ||| ||:: :||:|||| | :| | :| ||| |::: : |||| || :||
Db      7  FPEDEDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLDFQLMLKIRDTLYIAGRDQVYTV 64

Qy     80  DIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKNDDALFVCGTNA 139
      ::: | : |||||:| | : | ||||| ||||| : ||: |||||
Db     65  NLNEMPKEVI PNKKLTWRSRQQDRENCAMKGKHKDECHNFIKVFPVRNDEMVFVCGTNA 124

Qy    140  FNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAVIYR 199
      ||| || |:: || | :| ||:||||:|: | ||||| ||||| |||||
Db    125  FNPMCRYRLSTLEYDGEEISGLARCPFDARQTNVALFADGKLYSATVADFLASDAVIYR 184

Qy    200  SLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQVCK 259
      |:|: |||:|:||||:|:|: |::|:|:| ||||| ||| :|| | :||:|
Db    185  SMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYVFFFREIAVEHNNLGKAVYSRVARICK 244

Qy    260  NDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFSTPY 319
      ||||| ||||| ||||| ||||| |||:|:|:|:|:| | : | :|
Db    245  NDMGGSQRVLEKHWTSFLKARLNCSVPGDPFFYFDVLQSITDIIQINGIPTVVGVTTLQL 304

Qy    320  NSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYA 379
      ||||| ||:: | | || |||||:| | || |||:| ||||| || |
Db    305  NSIPGSAVCAFSMDIEKVFKGRFKEQKTPDSVWTAVPEDKVPKPRPGCCAKHGLAEAYK 364

Qy    380  TSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVF 439
      || :||:|:|:|:|:| || | : || :| ||||| |:|| :|||:|:|
Db    365  TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFTKTRVRYRLTAISVDHSAGPYQNYTVIF 424

Qy    440  LGSEKGIILKFLARIGNSGF-LNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASS 498
      :||| |:| | | : | |||: ||| || ||| : |||:: :||: :
Db    425  VGSEAGMVLKVLAK--TSPFSLNDSVLLLEEIEAYNHAKCSAENEEDKKVISLQLDKDHHA 482

Qy    499  LYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLT----- 552
      |||||:|:|:|:| |||:| |||:|||||||: : |:| :| |
Db    483  LYVAFSSCIIRIPLSRCERYGSCKKSCIASRDPYCGWLSQ-GSCGRVTPGMLLLTEDFFA 541

Qy    553  -----FEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGG-- 602
      :||| | || | |||| |:::| | | : ||
Db    542  FHNHSAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD-----YKIFGGPT 584

Qy    603  -----MLD-WKHL-----DSP---DSTDPLGAV 622
      :| | : | | | | :
Db    585  SDMEVSSSSVTTMASIPEITPKVIDTWRPKLTSSRKFFVQDDPNTSDFTDPLSGI 639
```

RESULT 6
US-09-254-594-6
; Sequence 6, Application US/09254594
; Patent No. 6566094

```
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Tissue Type: Child Brain
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-6
```

```
Query Match          27.9%; Score 1519.5; DB 4; Length 930;
Best Local Similarity 35.9%; Pred. No. 3.2e-135;
Matches 381; Conservative 135; Mismatches 356; Indels 189; Gaps 32;
```

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Qy      6 LLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMN 65
      ||| :| | | ||:| |: || | | : | : || | : :|
Db     13 LLLLLSLPH-TQAAFPQDPLPLISDLQGTSPLSWFRGLEDDAVAAEL-GLDFQRFLTLN 70

Qy     66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVL 124
      || :||| |::: |: | : :| |||:| : ||: | ::|| |||:|:|:|
Db     71 RTLLVAARDHVFSFDLQAEEEGGLVPNKYLTWRSQ--DVENCAVRGKLTDECYNYIRVL 128

Qy    125 LKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARC PYDAKHANVALFADGKLYS 184
      : : | |||:|:| ||:| : :| :| || |||:| : |||:|:| |||
Db    129 VPWDSQTL LACGTNSFS P VCRSYGITS LQ QEGEELSGQARCPFDATQSNVAIFAEGSLYS 188

Qy    185 ATVTDFLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYN 244
      || || | |||:| || | ||: |:| |||:|:|:|:|:|:|:|:|:|:|
Db    189 ATAADFQASDAVVYRSLGPQPPLRS AKYDSKWLREP HFVQALEHGDH VYFFFREVSVEDA 248

Qy    245 TMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIR 304
      :|| | |||:| ||| ||| | |: ||| ||| ||| ||| |||:|:|:| :
Db    249 RLGKVQFSRVARVCKRDMGGSFRALDRHWT SFLKLRLNCSVPGDSTFYFDVLQALTGPVN 308

Qy    305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERV PKP 364
      ::|| : |:| ||| ||| |||:| : :| | |:| |||:| | ||| ::|| |
Db    309 LHGRSALFGVFTTQ TNSIPGSAVCAFYLDEIERGFEGKFKEQ RSLDGAWTPVSEDRV P SP 368

Qy    365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA 424
      ||| ||| :::| : ||| | ||| |||:| ||| : :| | | ||:|
Db    369 RPGSCAGVGGAALFSSSRDL PDDVLT FIKAHPLLDPAVPPVTHQP-LLTLTSRALLTQVA 427

Qy    425 VDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVED 484
      || |||:| ||:| || | :|| | || | : : |||: |: :||
Db    428 VDG MAGPHSNITVMFLGSNDGTVLKVLTPGGRSGG-PEPILLEEIDAYSPARCSGKR TAQ 486
```

Qy 485 --KRIMGMLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGGAC 542
:|:|:|:| | | | | | | | | | | | | | | | | | |
Db 487 TARRIIGLELDTEGHRLFVAFSGCIVYLP LSR CARHGACQ R SCLASQDPYCGWHSSRG-C 545

Qy 543 SHLSPNSRLTFEQDIERGNTDGL--GDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR 600
: : : | | : : | | : : : | : : |
Db 546 VDIRGSGGTDVDQ---AGNQESMEHGDCQDG-----ATGSQSGPGDSAY--- 586

Qy 601 GGMLDWKHL L D S P D S T D P L G A V S S H N H Q D K K G V I R E S Y L K G H D Q L V P V T L L A I A V I L A F V 660
| | : : | | : | |
Db 587 -----GVRRDLPPASASRSVPIPLLLASVAAFA 615

Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRG-----SMSSVTKLSGL 708
:| | | | : | | | | | | | | | | : | : | | |
Db 616 LGASVSGLLVSCAC--RR-----AHRRRGKDIETPGLPRPLSLRSLARLHG- 659

Qy 709 FGDTQSKDKPKP--EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQ 766
| : | : | | : : | | : | | | | | | | |
Db 660 -GGPEPPPPSKDGDVQTPQLYTTFLPPPEGVPPP-----ELACLPTPESTPELPV 709

Qy 767 KRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSH-----IPSVVLPIT 821
| : | | | | | : | | : | | | | | | |
Db 710 KHLRAAGD-PWEWNQNRNNA-----KEGPGRSRGGHAAGGPAPRVLVRP-- 752

Qy 822 QQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHL----SSKSPNHGVNLVENLDS- 876
| | | : | | : | | : | | | | | | | |
Db 753 -----PPPGCPGQ-----AVEVTTL ELLRYLHGPQPPRKGAEPAPLTSR 793

Qy 877 -LPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLK 935
| | : | | | : | | : | | | | | | | | |
Db 794 ALPPE--PAPALLGGPSRPHECASPLRLDV-----PPEGRCASAPA---- 833

Qy 936 RNNTNSSNSSHL----SRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPS--- 988
| : : | | | | | | | | | | | | | | | |
Db 834 -RPALSAPAPRLGVGGRRLPFSGHRAPPALLTRV-----PSGGPSRYSGGPGKHL 883

Qy 989 --LNAYNSLTRSGLKRTPSLKPDPVPPKPSF-APLSTSMKPN 1026
| | | | | : | | | | | | | | | |
Db 884 LYLGRPEGYRGRALKRVDVEKPQLSLKPPLVGPSSRQAVPN 924

RESULT 7

US-09-254-594-3

; Sequence 3, Application US/09254594

; Patent No. 6566094

; GENERAL INFORMATION:

; APPLICANT: KIMURA, Toru

; APPLICANT: KIKUCHI, Kaoru

; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y

; FILE REFERENCE: 0020-4527P

; CURRENT APPLICATION NUMBER: US/09/254,594

; CURRENT FILING DATE: 1999-05-11

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 929

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; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Tissue Type: Brain
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-3
```

```
Query Match      26.2%; Score 1428.5; DB 4; Length 929;
Best Local Similarity 34.0%; Pred. No. 1.5e-126;
Matches 360; Conservative 147; Mismatches 355; Indels 197; Gaps 32;
```

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Qy      6 LLLYFTLLHFAGAGFPEDSEPISSHGNYSKQYPVFVGHKPGRNTTQRHRLDIQMIMIMN 65
      |||  |  |  ||:|  |:  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     11 LLLLLLSLPQAQTAFPDPIPLLTSDLQGTSPSSWFRGLEDDAVAAEL-GLDFQRFLTLN 69

Qy     66 GTLYIAARDHIYTVDDITSHT-EEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVL 124
      || :|||||::: |:  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     70 RTLLVAARDHVFSEFDLQAQEEGGLVPNKFLTWRSQ--DMENCAVRGKLTDECYNIYIRVL 127

Qy    125 LKKND DALFVCGTNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYS 184
      :  :  |  ||||:|:| ||:|  :  :|:  |:|  ||  ||||:|  |  ||:  |:|  |||
Db    128 VPWDSQTLLACGTNSFSPVCRSYGITSLQQEGEELSGQARCPFDATQSTVAISAEGSLYS 187

Qy    185 ATVTDFLAIDAVIYRSLGESPTLRVTKHDSKWLEKPYFVQAVDYGDIYFFFREIAVEYN 244
      ||  ||  |  |||:||||  |  ||:  |:||||:|  |  |::|:|:|  |  |::  :
Db    188 ATAADFQASDAVVYRSLGPQPPLRSKAYDSKWLEPHFVYALEHGDHVFYFFLPEKSL-WR 246

Qy    245 T--MGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDV 302
      |  |:|  |  |||:|  ||||  |  |::  |||||  |||||  ||||  |||:|:|:|
Db    247 TPGLGRVQFSRVARVCKRDMGGSRALDRHWTSLKLRNLCSVPGDSTFYFDVLQSLTGP 306

Qy    303 IRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDERVP 362
      :  ::||  :  |:|  |||||  ||||:  :  ||  |  |:|  |||:|  |  ||||  ::||
Db    307 VNLHGRSALFGVFTTQTNSIPGSAVCAFYLLDDIERGFEGKFKEQSRSLDGAWTPVSEDKVP 366

Qy    363 KPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTK 422
      ||||  |||  :  :::|  :  |||  |  |||  |||:|  |||  :|  |  |  ||:
Db    367 SPRPGSCAGVGAAALFSSSQDLDPDVLFFIKAHPLDPVPPATHQP-LLTLTSRALLTQ 425

Qy    423 IAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGV 482
      :|||  |||:|  ||:|  |||  |  :||  |  |  |  |  |  |  |  |  |  |  |
Db    426 VAVDGMAGPHRNTTVLFLGSNDGTVLKVLPP-GGQSLGPEPIILEEIDAYSHARCS--GK 482

Qy    483 ED----KRIMGMLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWIKE 538
      :||:|:|:|  |:||  |::  :  |  ||  |||  |:|:|:|  ||||  :
Db    483 RSPRAARRIIGLELDTEGHRFLVAFPGCIVYLSLRCARHGACQRSCLASLDPYCGWHRF 542

Qy    539 GGACSHLSPNSRLTFEQDIE-RGNTDGL--GDCHNSFVALNGHSSSLLPSTTTSDSTAQE 595
      |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    543 RGCVNIRGPGG-----TDVDLTGNQESMEHGDCQDG-----ATGSQSGPGDS 584

Qy    596 GYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPVTLIAIAV 655
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
```

Db 585 AY-----GVRRLSPASASRSIPIPLLLACV 610
 Qy 656 ILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSK 715
 || :|| ||: || | || : :|: ||: | : | |
 Db 611 AAALFALGASVSGLLVSCAC--RRAN----RRRSKDIETPGLPRPLSLRSLARLHGGGPEP 664
 Qy 716 DPKP---EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSR 772
 | | :| || :| | : :| ||||:| | | :
 Db 665 PPPPKDGDAAQTPQLYTTFLPPPEGGSPP-----ELACLPTPETTPELFPVKHLRAS 715
 Qy 773 GSREWERNQNLINACTKDMPPMGSPVIPTDLP---LRASPSHIPSVVVLPIITQQ---GYQ 826
 | || ||| || | | :| | | | : |
 Db 716 GG-PWEWNQNGNNASEGPRGRCSSAAGGPAPRVLRPPPGCPGQEVETTTLEELLRYL 774
 Qy 827 H-----EYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV 871
 | : :| || | || |
 Db 775 HGPQPPRKGSEPLASAPFTSRPPASEPGAALFVD-----SSPMR----- 814
 Qy 872 ENLDSLPP-----KVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVVDYKRSY 920
 | :|| | :| | | :| || :
 Db 815 ---DCVPPLRLDVPPDGKRAAPSGRPALSAPAPRLGVSG-SRRL-----PF 856
 Qy 921 PTNSLTRSHQATTLKRNNNTSSNSSHLNRNQSFGRGDNPPPPAPQRVDS--IQVHSSQPSG 978
 || :| || || | :| |
 Db 857 PT-----HRA-----PPGLLTRVPSGGPSRYSGGGPR 883
 Qy 979 QAVTVSRQPSLNAYNSLTRSGLKRTPSLKPVD--PPKPS 1015
 : : | | : || | :| | | : ||:|
 Db 884 HLLYLGR-PDGHGRSLKRVDVKSPKPLPLATPPQPA 921

RESULT 8

US-09-653-274-10

; Sequence 10, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 536

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-653-274-10

Query Match 25.3%; Score 1377.5; DB 4; Length 536;
 Best Local Similarity 49.3%; Pred. No. 4.1e-122;
 Matches 265; Conservative 97; Mismatches 167; Indels 9; Gaps 7;

```

Qy      6 LLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRRHRLDIQMIMIMN 65
      ||| :| | | ||:| |: || | | : | | | : :|
Db      4 LLLLLSLPH-TQAAFPQDPLPLLLISDLQTSPLSWFRGLEDDAVAAEL-GLDFQRFLTLN 61

Qy     66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVL 124
      || :||||:| : | : :| ||:| : || | :|| | | :| :|
Db     62 RTLLVAARDHVFSFDLQAEEEGGLVPNKYLTWRSQ--DVENCAVRGKLTDECYNYIRVL 119

Qy    125 LKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYS 184
      : : | |||:| : ||:| : :| | | |||:| | :||:| :| | |
Db    120 VPWDSQTLACGTNSFSPVCRSYGITSLQQEGEELSGQARCPFDATQSNVAIFAEGSLYS 179

Qy    185 ATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFFREIAVEYN 244
      || || | ||:| || | ||:| :| |||:| :| |||:| :| :| :| :|
Db    180 ATAADFQASDAVVYRSLGPQPPLRS AKYDSKWLREPHFVQALEHGDHVFYFFFREVSVEDA 239

Qy    245 TMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNC SVPGDSHFYFNILQAVTDVIR 304
      :|| | |||:| | || | | :| ||| | ||| | ||| :| :| :
Db    240 RLGKVQFSRVARVCKRDMGGSPRALDRHWT SFLKRLNC SVPGDSTFYFDVLQALTGPVN 299

Qy    305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERV PKP 364
      :|| : | :| ||| ||| : :| | | :||| :| | ||| :||| |
Db    300 LHGRSALFGVFTTQ TNSIPGSAVCAFYLDEIERGFEGKFKEQRS LDGAWTPVSED RVSP 359

Qy    365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFELRTMVRYRLTKIA 424
      ||| ||| :| : || | || | ||:| ||| : :| | | | :|
Db    360 RPGSCAGVGGAALFSSSRDLPDDVLTFIKAHPLLDPAVPPVTHQP-LLTLTSRALLTQVA 418

Qy    425 VDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVED 484
      || |||:| ||:| || | :|| | || | : :| ||| :| :|
Db    419 VDMAGPHSNITVMFLGSNDGTVLKVLTPGGRSGG-PEPILLEEIDAYSPARCSGKRTAQ 477

Qy    485 --KRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540
      :||:| :| | :||| | :| :| || || | :| :| :| :| |
Db    478 TARRIIGLELDTGHR LFVAFSGCIVYLP LSRCARHGACQRSCLASQDPYCGWHSSRG 535

```

RESULT 9

US-08-121-713D-58

; Sequence 58, Application US/08121713D

; Patent No. 5639856

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

```

; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-58

```

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Query Match          17.8%; Score 969.5; DB 1; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

```

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Qy      8 LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQR-----HRLDIQMI 61
| : || | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL 54

Qy     62 MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN 119
: : | : || : | : : | || : : | | | : | : || | : | |
Db     55 EKDHNSSLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy    120 FIKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV 174
: | : || | : || : : || || : | || : | | | | : | | : | |
Db    110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFPDPDHNST 165

Qy    175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYF 234
| : : : | : || || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    166 AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERS DLKQLNAPNFVNTMEYNDFIFF 220

Qy    235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFN 294
| | | | | | | | | | | | : : | | | : : : | | | | | | | | | | | | | | | |
Db    221 FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQGGDR-WTSFLKSRNLCSVPGDYPPFYFN 279

Qy    295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD 350
: | : : | | | | | : | : | | | | | | | : | | | | | | | : :
Db    280 EIQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSI LESFDGPFKEQETMN 339

```

Qy 351 STWTPVDPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
 | | | | : | : | | | | | | | | : | : | : | : | | | | : | | |
 Db 340 SNWLAVPSLKVPEPRPGQCVND-----SRTLDPVSVNFVKSHTLMDPAFFTRPI 391

Qy 411 FLRTMVRYRLTKIAVD---TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN----- 461
 : | : | : | | | | | | | | : | : | : | : | : | : | : | : | : | :
 Db 392 LIRISLQYRFTKIAVDQQVRTPDG--KAYDVLFIGTDDGKVIKAL----NSASFDSSDTV 445

Qy 462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
 | : : | : | | | | | | | | : | : | : | : | : | : | : | : | : | :
 Db 446 DSVVIEELQVLP-----PGVPVKNLYVVRMDGDDSKLVVVSDEILAIKLHRCGSDKIT 499

Qy 520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
 | : : | : : | | | | | | | | : | : | : | : | : | : | : | : | : | :
 Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy 576 NGHSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLDDSPDSTDPLGAVSSHNHQ 628
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 558 ----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy 629 DKKGVIRESYLKGHDQLVPV----TL-LAI-----AVILAFVMGAVFS 666
 | | | : : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 611 GSK-----LPSSQEKLPITYAETLTIAIVTSCLGALVVGFISGFLES 652

RESULT 10

US-08-835-268-58

; Sequence 58, Application US/08835268

; Patent No. 5807826

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,268

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713

; FILING DATE: 13-SEP-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 58:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 730 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-835-268-58

Query Match 17.8%; Score 969.5; DB 1; Length 730;
 Best Local Similarity 34.4%; Pred. No. 5.7e-83;
 Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

Qy	8	LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQR-----HRLDIQMI	61
		: : : ::	
Db	11	LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL	54
Qy	62	MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHN	119
		: : : : : : : : : : :	
Db	55	EKDHNSSLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYIKGKSEDDCQN	109
Qy	120	FIKVLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV	174
		: : : : : : : : : : : :	
Db	110	YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFDPDHNST	165
Qy	175	ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYF	234
		: : : : : : : : :	
Db	166	AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERSDLKQLNAPNFVNTMEYNDFIFF	220
Qy	235	FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPGDSHFYFN	294
		: : : : : : : : : :	
Db	221	FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQGGDR-WTSFLKSRLNCVPGDYPFYFN	279
Qy	295	ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD	350
		: : : : : : : : :	
Db	280	EIQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSILESFDGPFKEQETMN	339
Qy	351	STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW	410
		: : : : : : :	
Db	340	SNWLAVPSLKVPEPRPGQCVND-----SRTLDPVSVNFVKSHTLMDEAVPAFFTRPI	391
Qy	411	FLRTMVRYLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN-----	461
		: : : : : : : : : :	
Db	392	LIRISLQYRFETKIAVDQQVPTPDG--KAYDVLFIGTDDGKVIKAL----NSASFDSSDTV	445
Qy	462	DSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG	519
		: : : : : : : : : : :	
Db	446	DSVVIIEELQVLP-----PGVPVKNLYVVRMDGDDSKLVVVSDDDEILAIKLRHRCGSDKIT	499
Qy	520	KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL	575
		: : : : : : : : : : : :	

Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy 576 NGHSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLLDSPDSTDPLGAVSSSHNHQ 628
 :| :|: |: |: | :| :| :| :|: || :|: ||

Db 558 ----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy 629 DKKGVIRESYLKGHDLVLPV----TL-LAI-----AVILAFVMGAVFS 666
 | :|: || :|| |:: |: | :||

Db 611 GSK-----LPSSQEKLPITYAETLTIAIVTSCILGALVVGFI SGFLFS 652

RESULT 11

US-09-060-692-58

; Sequence 58, Application US/09060692

; Patent No. 5935865

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/060,692

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713

; FILING DATE: 13-SEP-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: B94-002-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; TELEX:

; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 730 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-060-692-58

Query Match 17.8%; Score 969.5; DB 2; Length 730;
 Best Local Similarity 34.4%; Pred. No. 5.7e-83;
 Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

```

Qy      8 LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNNTQR-----HRLDIQMI 61
      | : || | : | | | | | | | | | | | | | | | | : ::
Db     11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL 54

Qy     62 MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN 119
      : : | : || : | : : | || : : : | | | : | : || : | |
Db     55 EKDHNSLLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy    120 FIKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV 174
      : : || | : || : : || || : | || : | | | : | : || : | :
Db    110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFPDPHNST 165

Qy    175 ALFADGKLYSATVTD FLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYGDYIYF 234
      | : : : | : || || | | : || | || : | | | | | | : : | | : |
Db    166 AIYSEGLYSATVADFSGTDPLIYRG-----PLRTERS DLKQLNAPNFVNTMEYNDFIFF 220

Qy    235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFN 294
      | || | || | | : : || : || : | | : : : || || : || || || | || |
Db    221 FFRETAVEYINCGKAIYSRVARVCKHDKGQPHQGGDR-WTSFLKSRLNCSVPGDYPFYFN 279

Qy    295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD 350
      : | : : | | | | : : | : || || || || || : | | | || : : :
Db    280 EIQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSILESFDGPFKEQETMN 339

Qy    351 STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
      | | || : || : || | | | | | | | | : || : | : | || || : | |
Db    340 SNWLAVPSLKVPEPRPGQCVND-----SRTLDPVSVNFVKSH TLMDEAVPAFFT RPI 391

Qy    411 FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN----- 461
      : | : : || || || | | : : | : | : : | : | | | | :
Db    392 LIRISLQYRFTKIAVDQQV RTPDG--KAYDVLFIGTDDGKVIKAL----NSASFSSDTV 445

Qy    462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
      || : : || : | | | | : : : | | | : : : | | | :
Db    446 DSVVIEELQVLP-----PGVPVKNLVVRMDGDDSKLVVVSDD EILAIKLHRCGSDKIT 499

Qy    520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
      | : : | : : || || | | : : || : : | | | | | | : :
Db    500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy    576 NGHSSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHL LDSPDSTDPLGAVSSHNHQ 628
      : | : : | : | : | : | : : : | | : : | |
Db    558 ----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy    629 DKKGVIRESYLKGH DQLV PV----TL-LAI-----AVILAFVMGAVFS 666
      | | : : | | : || | : : : | : | : |
Db    611 GSK-----LPSSQEKLPIYTAETLTIAIVT SCLGALVVGFI SGFLFS 652

```

RESULT 12
 US-08-833-391-58
 ; Sequence 58, Application US/08833391

```

; Patent No. 6013781
; GENERAL INFORMATION:
;   APPLICANT: Goodman, Corey S.
;   APPLICANT: Kolodkin, Alex L.
;   APPLICANT: Matthes, David
;   APPLICANT: Bentley, David R.
;   APPLICANT: O'Connor, Timothy
;   TITLE OF INVENTION: The Semaphorin Gene Family
;   NUMBER OF SEQUENCES: 100
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;     STREET: 268 Bush Street, Suite 3200
;     CITY: San Francisco
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94104
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/833,391
;     FILING DATE:
;     CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/121,713
;     FILING DATE: 13-SEP-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Osman, Richard A.
;     REGISTRATION NUMBER: 36,627
;     REFERENCE/DOCKET NUMBER: B94-002-1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415)343-4341
;     TELEFAX: (415) 343-4342
;     TELEX:
;   INFORMATION FOR SEQ ID NO: 58:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 730 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-833-391-58

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Query Match          17.8%; Score 969.5; DB 3; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

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Qy      8 LYF'TLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQR-----HRLDIQMI 61
      | : || | : | | | | | | | | | | | | | | | | : ::
Db     11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL 54

Qy     62 MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN 119
      : : | : || : | : : | || : : | | | : | : || : | : |
Db     55 EKDHNSLLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy    120 FIKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV 174

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      :|:| | :| : :| | | : | | : | : | : | : | :
Db      110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFPDPHNST 165

Qy      175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYF 234
      |:::|:| | | | | | | | :| | | | | | | :| | :| :| :|
Db      166 AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERSDLKQLNAPNFVNTMEYNDFIFF 220

Qy      235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFN 294
      | | | | | | | | :| :| :| :| :| :| :| :| :| :| :| :|
Db      221 FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQGGDR-WTSFLKSRNCSVPGDYPPYFN 279

Qy      295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD 350
      :| :| :| | | | : | :| | | | | | | :| | | | :| :| :
Db      280 EIQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSILESFDGPFKEQETMN 339

Qy      351 STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
      | | | | :| :| | | | | | | | :| :| :| :| | | | | :| |
Db      340 SNWLAVPSLKVPEPRPGQCVND-----SRTLDPVSVNFVKSHTLMDEAVPAFFTRPI 391

Qy      411 FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN----- 461
      :| :| :| | | | | | | :| :| :| :| :| :| :| :| :| :
Db      392 LIRISLQYRETKIAVDQQVVRTPDG--KAYDVLFIGTDDGKVIKAL----NSASFSSDTV 445

Qy      462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
      | | :| :| | | | | | | :| :| :| :| | | | :| :| :| :
Db      446 DSVVIEELQVLP-----PGVPVKNLYVVRMDGDDSKLVVSDDEILAIKLHRCGSDKIT 499

Qy      520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
      | :| :| :| | | | | | :| :| :| :| :| :| :| :| :| :
Db      500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy      576 NGHSSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQ 628
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :
Db      558 ----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy      629 DKKGVIRESYLKGHDLQVLPV----TL-LAI-----AVILAFVMGAVFS 666
      | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :
Db      611 GSK-----LPSSQEKLPITYAETLTIAIVTSCLGALVVGFI SGFLFS 652

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RESULT 13

US-09-060-610-58

; Sequence 58, Application US/09060610

; Patent No. 6344544

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

```

; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,268
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-060-610-58

```

```

Query Match          17.8%; Score 969.5; DB 4; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

```

```

Qy      8 LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNNTTQR-----HRLDIQMI 61
      | : || | : | | | | | | | | | | | | | | | | : ::
Db     11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL 54

Qy     62 MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN 119
      : : | : || : | : : | || : : : | | | : | : || : | : |
Db     55 EKDHNSLLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy    120 FIKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFGSMARCPYDAKHANV 174
      : || || | : || : : || || : | || : | : | | : | : |
Db    110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFDPDHNST 165

Qy    175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYIF 234
      | : : : | : || || | | | : || | || : | | | | | | : | : | : |
Db    166 AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERSCLKQLNAPNFVNTMEYNDFIFF 220

Qy    235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFN 294
      || || || || | : : || : || : | : : || || || : || || || || || ||
Db    221 FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQGGDR-WTSFLKSRLNCSVPGDYPFYFN 279

Qy    295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD 350
      : : : : | | | : | : || || || || || : | | | | || : : :
Db    280 EIQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSIKSFDFGPFKEQETMN 339

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Qy 351 STWTPVPPERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
 | | | | : | : | | | | | | | | : | : | : | : | | | | | : | | |
 Db 340 SNWLAVPSLVPEPRPGQCVND-----SRTLPDVSVNFVKSHTLMDPAFFTRPI 391

Qy 411 FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN----- 461
 : | : : | | | | | | | | : : | : | : | : | : | : | : | : | :
 Db 392 LIRISLQYRFTKIAVDQQVVRTPDG--KAYDVLFIGTDDGKVIKAL----NSASFDSSDTV 445

Qy 462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
 | : : | : | | | | | | : : | : | : | : | : | : | : | : | :
 Db 446 DSVVIEELQVLP-----PGVPVKNLVVRMDGDDSKLVVVSDEILAIKLRHRCGSDKIT 499

Qy 520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
 | : : | : : | | | | | | : : | : | : | : | : | : | : | : | :
 Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy 576 NGHSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLDDSPDSTDLGAVSSHNHQ 628
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 558 ----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy 629 DKKGVIRESYLKGHDQLVPV----TL-LAI-----AVILAFVMGAVFS 666
 | | | : : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 611 GSK-----LPSSQEKLPIYTAETLTIAIVTSCLGALVVGFI SGFLFS 652

RESULT 14

PCT-US94-10151A-58

; Sequence 58, Application PC/TUS9410151A

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/10151A

; FILING DATE: 13-SEP-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299 FHT UR

```
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 730 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US94-10151A-58
```

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Query Match          17.8%; Score 969.5; DB 5; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;
```

```
Qy      8 LYFTLLHFAGAGFPEDESEPI SISHGNYTKQYPVFVGHKPGRNTTQR-----HRLDIQMI 61
      | : || | : | | | | | | | | | | | | | | | | : ::
Db     11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL 54

Qy     62 MIMNGTLYIAARDHIYTVDDID--TSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHN 119
      : : | : || : | : : | || : : | | | : | : || : | : |
Db     55 EKDHNSLLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKKGKSEDDCQN 109

Qy    120 FIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV 174
      : : || | : || : : || || : | || : | | : | | : |
Db    110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFDPDHNST 165

Qy    175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRVTKHDSKWLKEPYFVQAVDYGDIYIF 234
      | : : : | : || || | | | : || | | | : | | | | : | : | : |
Db    166 AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERSCLKQLNAPNFVNTMEYNDFIFF 220

Qy    235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFN 294
      || || || || | | : : || : || : | | : : || || || || || || || ||
Db    221 FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQGGR-WTSFLKSRLNCSVPGDYFFYFN 279

Qy    295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD 350
      : | : : | | | | : | : || || || || || : | | | | || : : :
Db    280 EIQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSILESFDGPFKEQETMN 339

Qy    351 STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
      | | || : | : || || | | | | | | : | | : | : | : | | || ||
Db    340 SNWLAVPSLKVPEPRPGQCVND-----SRTLDPVSVNFVKSHTLMDEAVPAFFTRPI 391

Qy    411 FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN----- 461
      : | : : || || || || | | : : | : | : : | : | | | :
Db    392 LIRISLQYRFTKIAVDQQVRTPDG--KAYDVLFIGTDDGKVIKAL----NSASFDSSTV 445

Qy    462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
      || : : || : | | | | : : : | | | : : : | || : :
Db    446 DSVVIEELQVLP-----PGVPVKNLVVRMDGDDSKLVVVSDDDEILA IKLHRCGSDKIT 499

Qy    520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
      | : : | : : || || | | : : || : | : | | | : :
Db    500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy    576 NGHSSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLDSPDSTDPLGAVSSHNHQ 628
      : | : : | : | : | : | : : : | | : : ||
Db    558 ----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy    629 DKKGVIRESYLKGHDLVPV----TL-LAI-----AVILAFVMGAVFS 666
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Db 611 GSK-----LPSSQEKLPITYTAETLTIAIVTSCLGALVVGFI SGFLFS 652

RESULT 15

US-08-121-713D-60

; Sequence 60, Application US/08121713D

; Patent No. 5639856

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713D

; FILING DATE: 13-SEP-1993

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: B94-002-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415)343-4341

; TELEFAX: (415) 343-4342

; TELEX:

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 650 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-121-713D-60

Query Match 16.1%; Score 880; DB 1; Length 650;

Best Local Similarity 35.8%; Pred. No. 1.6e-74;

Matches 207; Conservative 95; Mismatches 194; Indels 82; Gaps 19;

Qy 114 KDECHNFIKVLKKNDDALFVCGTNAFNPSCRNYKMD----TLEPFGDEFSGMARCPYDA 169

:|:| |:|::: : |||||:| | | : ||| :| | |||

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Qy 170 KHANVALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYG 229

```

      :| : :: || :||| || || | :||| | :| ::|| | | || : |
Db      58 RHNSTSVLADNELYSGTVADFSGSDPIIYRE-----PLQTEQYDSLNLNAPNFVSSFTQG 112

Qy      230 DYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQVRVLEKQWTSFLKARLNCSVPGDS 289
      |: :||| ||| : || : : |||: || | || | :||| |: ||| :|||
Db      113 DFVYFFFRETAVEFINCGKAIYSRVARVCKWDKGGPHR-FRNRWTSFLKSRLNCSIPGDY 171

Qy      290 HFYFNILQAVTDVIR----INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKE 345
      |||| :|: :: : : : : ||| ||| ||| : : ||| | |: |||
Db      172 PFYFNEIQSASNLVEGQYGSMSKLIYGVFNTSPNSIPGSAVCAAFALQDIADTFEGQFKE 231

Qy      346 QKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSI 405
      | :| | || : :|| |||| | : | || ||||| |||| ||:
Db      232 QTGINSNWLPVNNAKVPDPRPGSC-----HNDSRALPDPTLNFIKTHSLMDENVPAF 283

Qy      406 FNRPWFLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFL-ARIGNSGFL 460
      |: :| :|| || |: ||| | | : : |: |: : : | |: | : | :|
Db      284 FSQPILVRTSTIYRFTQIAVDAQIKTPGG--KTYDVIFVGTDHGKIIKSVNAESADSADK 341

Qy      461 NDSLFLLEMSVYNSEKCSYDGVEDKRIM-GMQLDRASSSLY-----VAFSTCVIKVPLG 513
      |: :||: | : : : |: || |: | : : |: : : |
Db      342 VTSVVIEEIDVLTKS----EPIRNLEIVRTMQYDQPKDGSYDDGKLIIVTDSQVVAIQ LH 397

Qy      514 RC--ERHGKCKKTCIASRDPYCGWIKEGGAC-SHLSPN--SRLTFEQDIERGNTDGLGDC 568
      || :: | : |:| :||| | | | || :| | |: |
Db      398 RCHNDKITSCSE-CVALQDPYCAWDKIAGKCRSHGAPRWLEENYFYQNVATGQ----- 449

Qy      569 HNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSH NHQ 628
      |: : : : |: | | | | ||| |
Db      450 -----HAACPSGKINSKDANAGEQKGFRNDM----DLLDS-----RRQ 483

Qy      629 DKKGVIRESYLKGHDLVPVTLLAIAVILAFVMGAVFS 666
      | | : : | : : : : :| : |: ||
Db      484 SKDQEIIDNIDKNFEDIINAQYTVETLVMAGVLAGSIFS 521

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Search completed: March 24, 2004, 13:17:59
Job time : 36.7132 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:11:23 ; Search time 30.8439 Seconds
(without alignments)
3212.214 Million cell updates/sec

Title: US-09-856-681A-2
Perfect score: 5450
Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	971.5	17.8	730	2	JH0798	fasciclin IV precu
2	875	16.1	656	2	B49423	semaphorin I - fru
3	852.5	15.6	771	2	D49423	semaphorin III pre
4	845.5	15.5	711	2	A49423	semaphorin I precu
5	842.5	15.5	772	2	I48747	semaphorin D - mou
6	839.5	15.4	772	2	A49069	collapsin - chicke
7	830	15.2	1074	2	JC5928	semaphorin F precu
8	826	15.2	749	2	G01856	semaphorin V - hum
9	803	14.7	748	2	I48744	semaphorin A - mou
10	793.5	14.6	666	2	I58169	semaphorin III - m
11	789	14.5	712	2	T27165	hypothetical prote
12	779.5	14.3	724	2	C49423	semaphorin II prec
13	768	14.1	753	2	G02173	semaphorin III fam

14	737	13.5	751	2	I48748	semaphorin E - mou
15	692	12.7	834	2	S66498	M-sema F protein p
16	656	12.0	782	2	I48746	semaphorin C - mou
17	641.5	11.8	760	2	I48745	semaphorin B - mou
18	356.5	6.5	653	2	T03102	semaphorin homolog
19	322.5	5.9	676	2	T33853	hypothetical prote
20	238	4.4	1945	2	T13937	plexin A - fruit f
21	217	4.0	403	2	E42521	A39R protein - vac
22	208	3.8	441	2	S29921	hypothetical prote
23	199.5	3.7	1884	2	JC4975	plexin 2 precursor
24	182	3.3	1905	2	I51553	Plexin - African c
25	163.5	3.0	3968	2	A44265	trithorax homolog
26	158	2.9	2051	2	T13164	plexin B - fruit f
27	155.5	2.9	1894	2	JC4980	plexin 1 precursor
28	155	2.8	1375	1	JC5148	hepatocyte growth
29	155	2.8	2352	2	T30201	Notch homolog prot
30	153	2.8	625	2	S48941	regulatory protein
31	147.5	2.7	3507	2	T34513	hypothetical prote
32	147	2.7	1425	2	T30811	hepatocyte growth
33	146.5	2.7	295	2	JQ1775	SalL9R protein - v
34	140	2.6	1390	1	TVHUME	hepatocyte growth
35	139.5	2.6	3869	2	A48205	All-1 protein +GTE
36	138.5	2.5	1065	2	S19482	hypothetical prote
37	138	2.5	728	2	S48569	hypothetical prote
38	137	2.5	867	2	T41308	hypothetical zinc-
39	137	2.5	2492	1	C44213	nonstructural poly
40	136.5	2.5	1347	2	T02214	ubiquitous TPR mot
41	136	2.5	1310	2	T40135	oxysterol-binding
42	136	2.5	2531	2	S18188	notch protein homo
43	133.5	2.4	1829	2	T14280	RW1 protein - mous
44	133.5	2.4	2187	2	T30826	nascent polypeptid
45	133.5	2.4	2531	2	A46019	notch-1 protein -

ALIGNMENTS

RESULT 1

JH0798

fasciclin IV precursor - American bird grasshopper

C;Species: Schistocerca americana (American bird grasshopper)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: JH0798

R;Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Goodman, C.S.

Neuron 9, 831-845, 1992

A;Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in the grasshopper embryo.

A;Reference number: JH0798; MUID:93040225; PMID:1418998

A;Accession: JH0798

A;Molecule type: mRNA

A;Residues: 1-730 <KOL>

A;Cross-references: GB:L00709; NID:g160844; PID:g160845

A;Experimental source: embryo

C;Comment: This protein plays a role in growth cone guidance in the developing central nervous system.

C;Keywords: glycoprotein; transmembrane protein

```
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-730/Product: fasciclin IV #status predicted <MAT>
F;23-627/Domain: extracellular #status predicted <EXT>
F;628-652/Domain: transmembrane #status predicted <TMM>
F;653-730/Domain: intracellular #status predicted <INT>
F;44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status
predicted
```

Qy	8	LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGPRNTTQR-----HRLDIQMI	61
Db	11	LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL	54
Qy	62	MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHN	119
Db	55	EKDHNSLLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN	109
Qy	120	FIKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV	174
Db	110	YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD---GDYVVEKEYEGRGLCPFDPDHNST	165
Qy	175	ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYIF	234
Db	166	AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERSDLKQLNAPNFVNTMEYNDFIFF	220
Qy	235	FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFN	294
Db	221	FFRETAVEYINCGKAIYSRVARVCKHKDKGGPHQFGDR-WTSFLKSRLNCSVPGDYPFYFN	279
Qy	295	ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD	350
Db	280	EIQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSI LESFDGPFKEQETMN	339
Qy	351	STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW	410
Db	340	SNWLAVPSLKVPEPRPGQCVND-----SRTL PDVS VNFVKSHTLMDEAVPAFFTRPI	391
Qy	411	FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN-----	461
Db	392	LIRISLQYRFTKIAVDQQV RTPDG--KAYDVLFIGTDDGKVIKAL---NSASFDSSTV	445
Qy	462	DSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG	519
Db	446	DSVVIEELQVLP-----PGVPVKNLVVRMDGDDSKLVVVSDEILAIKLHRCGSDKIT	499
Qy	520	KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL	575
Db	500	NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV-	557
Qy	576	NGHSSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHL L D S P D S T D P L G A V S S H N H Q	628
Db	558	----ASPVPTQPTTKSSGDPVHSIHQA E FEPE---IDNEIVIGVDDSNVIPNTLAEINHA	610
Qy	629	DKKGVIRESYLKGHDQLVPV----TL-LAI-----AVILAFVMGAVFS	666

Db 611 GSK-----LPSSQEKLPITYAETLTIAIVTSCLGALVVGFI SGFLFS 652

RESULT 2

B49423

semaphorin I - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999

C;Accession: B49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A;Reference number: A49423; MUID:94094332; PMID:8269517

A;Accession: B49423

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-656 <KOL>

A;Cross-references: GB:L26082

C;Genetics:

A;Gene: semaI

A;Cross-references: FlyBase:FBgn0011259

Query Match 16.1%; Score 875; DB 2; Length 656;
Best Local Similarity 35.6%; Pred. No. 1.4e-50;
Matches 208; Conservative 95; Mismatches 193; Indels 88; Gaps 20;

Qy 114 KDECHNFIKVLKKNDDALFVCGTNAFNPSCRNYKMD----TLEPFGDEFSGMARCPYDA 169
:|:| |:|::: : |||||:| | | : || | | | |
Db 1 EDDCQNYIRIMVVPSPGRLFVCGTNSFRPMCNTYIISDSNYTLEA---TKNGQAVCPYDP 57

Qy 170 KHANVALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYG 229
:| : :: || :|| | | | | :|| | :| :|| | | | : |
Db 58 RHNSTSVLADNELYSGTVADFSGSDPIIYRE-----PLQTEQYDSLNLNAPNFVSSFTQG 112

Qy 230 DYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDS 289
|::| ||||| |||: || :: |||:| | | | :||| | :||| :||
Db 113 DFVYFFFRETAVEFINCGKAIYSRVARVCKWDKGGPHR-FRNRWTSFLKSRNLNCSIPGDY 171

Qy 290 HFYFNILQAVTDVIR----INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKE 345
||| :|: :::: : : |:|| ||||| | : : || | | :|||
Db 172 PFYFNEIQSASNLVEGQYGSMSKLIYGVFNTPSNSIPGSAVCAFALQDIADTFEGQFKE 231

Qy 346 QKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSI 405
| :| | | | : :|| |||| | : | | ||||| |||| | :
Db 232 QTGINSNWLPVNNAKVPDPRPGSC-----HNSRALPDPTLNFIKTHSLMDENVPAP 283

Qy 406 FNRPWFLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFL-ARIGNSGFL 460
|::| :|| | | | :||| | | : : |:|:|: | |:| : | :|
Db 284 FSQPILVRTSTIYRFTQIAVDAQIKTPGG--KTYDVI FVGTDHGKIIKSVAESADSADK 341

Qy 461 NDSLFLLEMSVYNSEKCSYDGVEDKRIM-GMQLDRASSSLY-----VAFSTCVIKVPLG 513
|: :||: | : : : |: || | : | : : | : : |
Db 342 VTSVVEEIDVLTKS----EPIRNLEIVRTMQYDQPKDGSYDDGKLIIVTDSQVVAIQLH 397

```

Qy      514 RC--ERHGKCKKTCIASRDPYCGWIKEGGAC-SHLSPN--SRLTFEQDIERGNTDGLGDC 568
      ||  ::  | : |:| :||| | | | | | :|  | |::  |
Db      398 RCHNDKITSCSE-CVALQDPYCAWDKIAKGCRSHGAPRWLEENYFYQNVATGQ----- 449

Qy      569 HNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLDSPDSTDPLGAVSSSHNHQ 628
      |::      : |: | ||  | |  |||  |  |
Db      450 -----HAACPSGKINSKDANAGEGKGFRNDM----DLLDS-----RRQ 483

Qy      629 DKKGVIRESYLKGHD-----QLVPVTLIAIAVILAFVMGAVFS 666
      |  | ::  | :      ::      ::| : |::|
Db      484 SKDQEIIDNIDKNFEGPQTSADIINAQYTVETLVMAGSIFS 527

```

RESULT 3

D49423

semaphorin III precursor - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999

C;Accession: D49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A;Reference number: A49423; MUID:94094332; PMID:8269517

A;Accession: D49423

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-771 <KOL>

A;Cross-references: GB:L26081; NID:g799328; PIDN:AAA65938.1; PID:g436560

C;Genetics:

A;Gene: GDB:SEMA1

A;Cross-references: GDB:283448

C;Superfamily: semaphorin

```

Query Match          15.6%;  Score 852.5;  DB 2;  Length 771;
Best Local Similarity 32.1%;  Pred. No. 5.8e-49;
Matches 208;  Conservative 106;  Mismatches 250;  Indels 83;  Gaps 20;

```

```

Qy      44 HKPGRNTTQRHRLDIQMIMIMNGT-----LYIAARDHIYTVD 80
      :: |:|  | :| : ::  |  ||: |:|::|
Db      22 YQNGKNNVPRKLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHIFSFD 81

Qy      81 IDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKH-KDECHNFIKVLKKND DALFVCGTNA 139
      :  |  ::|  | | :  ||  || |||||  |  | : ||| |
Db      82 L-----VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGA 136

Qy      140 FNPSCR-----NYKMDTLEPGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLA 192
      |:| |  ::  | :  :  :| : ||| |  :| ||:| | | ||:
Db      137 FHPICTYIEIGHHPEDNIFKLENSHFENGGRGKSPYDPKLLTASLLIDGELYSGTAADFMG 196

Qy      193 IDAVIYRSLGESPTLRVTKHDSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNT 245
      |  |:|:|  :|| :||:| :| | :  |  :| ||||| |::
Db      197 RDAIFRTLGHHHPIRTEQHDSRWLNDPKFISAHLISESDNPEDDKVYFFFRENAIDGEH 256

Qy      246 MGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPG----DSHFYFNILQAVTD 301
      ||  | : |:| | | | | :|:| | | | | | | | :| |  : |
Db      257 SGKATHARIGQICKNDFGG-HRSLVNKWTTF LKARLICSVPGPNGIDTHF-----DELQD 310

```



```

      :|      | :|||:| || |      : : | | : |||: :| : : :|:
Db      111 ILYSSEPGKLVICGTNSYKPLCRTYAFKEGKYLVEKEVEGIGLCPYNPEHNSTSVSYNGQ 170

Qy      182 LYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAV 241
      |:|||| || | :|||      || | | | | || :| |||||:|:| ||
Db      171 LFSATVADFSGGDPLIYRE-----PQRTSLDLKQLNAPNFVNSVAYGDYIFFFYRETAV 225

Qy      242 EYNTMGKVVFPRAQVCKNDMGGSQVRLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTD 301
      || |||:| |||:|:| || : : : ||||| |||||:|:| |||: :|: :|
Db      226 EYMNCGKVIYSRVARVCKDDKGGPHQSRDR-WTSFLKARLNCSIPGEYPFYFDEIQSTSD 284

Qy      302 VI--RINGRD--VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
      :: | | | : : :|| :| |||:| || | || | || |: :| | |||
Db      285 IVEGRYNSDDSKIYIGILTPVNAIGGSAICAYQMADILRVFEGSFKHQETINSNWLVPV 344

Qy      358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
      ||:|||| | | :      || :||||| ||:| ||:| :| :| : :
Db      345 QNLVPEPRPGQCVRDSRI-----LPDKNVNFIKTHSLMED-VPALFGKPVLRVSLQ 395

Qy      418 YRLTKIAVDTAAGPYQNH--TVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNSE 475
      || | | || | | :|:|:| :| :||
Db      396 YRFTAITVDPQVKTINNQYLDVLYIGTDDGKVLK----- 429

Qy      476 KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCV-----IKVP----- 511
      : : | : || : | | :|:
Db      430 -----AVNIPKRHAKALLYRKYRTSVHHPHGAPVKQLKIAPGYGKVVVVGKDEIR 478

Qy      512 ---LGR CERH GKCKKTCIASRDPYCGWIKGACSHLSPNSRLTF-EQDIERN----- 561
      | | :| | | :|:| | : | : : | ||:|:
Db      479 LANLNHCASKTRC-KDCVELQDPHCAWDAKQNLCSIDTVTSYRFLIQDVVRGDDNKCWS 537

Qy      562 --TDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPL 619
      || | | || : : | :| | | ||:| ||
Db      538 PQTDKKTVIKNK-----PSEVENEIT-----NSIDEKDL---DSSDPL 572

Qy      620 GAVSSHNHQQDKKGVIRESYLKG---HDQLVPVT--LLAIAVILAFVMGA---VFSGITVY 671
      : | | | : : | || | | | : : :| :|:|:|:
Db      573 IKTGLDDSDCDPV-SENSIGGCAVRQQLVIYTAGTLHIVVVVVSIVGLFSWLYSGLSVF 631

Qy      672 CV--CDHRRKDVAVVQRKE--KELTHSRRGSMS-SVTKLSGLFGDTQSKDPKPEAILTPL 726
      | : : : : :|: : : | : : | | | | |:|: :
Db      632 AKFHSDSQYPEAPFIEQHNHLERLSANQTGYLTFRANKAVNLVVKVSSSTPRPKKDNLDV 691

Qy      727 MHNGKLATPGNTAKM 741
      : :|: | | :
Db      692 SKDLNIASDGTLQKI 706

```

RESULT 5

I48747

semaphorin D - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C;Accession: I48747

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.
A;Reference number: I48744; MUID:95267431; PMID:7748561
A;Accession: I48747
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-772 <RES>
A;Cross-references: EMBL:X85993; NID:g854329; PIDN:CAA59985.1; PID:g854330
C;Genetics:
A;Gene: semD
C;Superfamily: semaphorin

Query Match 15.5%; Score 842.5; DB 2; Length 772;
Best Local Similarity 34.3%; Pred. No. 2.7e-48;
Matches 200; Conservative 85; Mismatches 225; Indels 73; Gaps 16;

```

Qy      47 GRNTTQRHRLDIQMIMMNGT-----LYIAARDHIYTVDIDT 83
      |:| | :| : :: | | :| :||| : :
Db      25 GKNNVPRCLKLSYKEMLESNNVITFENGLANSSSYHTFLLDEERSRLYVGAKDHIFSFLN-- 82

Qy      84 SHTEEIYCSKKLTWKSQRQADVDTCRMKGKH-KDECHNFIKVLLKKNDDALFVCGTNAFNP 142
      | :| : | | : || || |||| | | :| ||| ||:|
Db      83 ---VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLEAYNQTHLYACGTGAFHP 139

Qy     143 SCR-----NYKMDTLEPFGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLAIDA 195
      | : : | : | :| : ||| | :| ||:| | | :|
Db     140 ICTYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLLIDGELYSGTAADFMRGRDF 199

Qy     196 VIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGK 248
      |:|:| : || :|||:| :| :| | :||| | : ||
Db     200 AIFRTLGDHHPIRTEQHDSRWLNDPRFISAHLIPESDNPEDDKVYFFFRENAIGGEHSGK 259

Qy     249 VVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPG----DSHFYFNILQAVTDVIR 304
      |:|:| | | | :| :||:| | | | | | :| :| :|
Db     260 ATHARIGQICKNDFGG-HRSLVNKWTTFLKARLICSVPGPNGIDTHF-----DELQDVFL 313

Qy     305 INGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
      :| :| :| :| | | | | | | :| | : :| :| |
Db     314 MNSKDPKNPIVYGVFTTSSNIFKGSAVCMYSMSDVRVFLGPYAHRDGPYQWVPY-QGR 372

Qy     361 VPKPRPGCCAGSSSLERYATSNEFPDDLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
      || ||| | | : : : : || :| :|| | | | ||| :| | :|
Db     373 VPYPRPGTCP-SKTFGGFDSTKDLRDDVITFGRSHPAMYNPVFPINNRPIMIKTDVNYQF 431

Qy     421 TKIAVDTAAGPYQNHTVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
      |:| || :| :|:| :| :|| : : : :| :| :|
Db     432 TQIVVDRVDAEDGQYDVMFIGTVDGTVLVKVVSPKETWHDLEEVLLLEEMTVFR----- 484

Qy     481 GVEDKRIMGMQLDRASSSLYVAESTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWIKEGG 540
      | | | :| || : | :|| || :|| | :||| | :|
Db     485 --EPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECLARDPYCAW--DGS 540

Qy     541 ACSHLSPNS-RLTFEQDIERGNTDGLGDCHNSFVALNGHSSSL 582
      :|| | :| | || | | | : | | ||
Db     541 SCSRYFPTAKRRTRRQDIRNG--DPLTHCSDLEDHNDHHGPSL 581

```

RESULT 6
 A49069
 collapsin - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999
 C;Accession: A49069
 R;Luo, Y.; Raible, D.; Raper, J.A.
 Cell 75, 217-227, 1993
 A;Title: Collapsin: a protein in brain that induces the collapse and paralysis
 of neuronal growth cones.
 A;Reference number: A49069; MUID:94006554; PMID:8402908
 A;Accession: A49069
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-772 <LUO>
 A;Cross-references: GB:U02528; NID:g410078; PIDN:AAC59638.1; PID:g410079
 C;Superfamily: semaphorin

Query Match 15.4%; Score 839.5; DB 2; Length 772;
 Best Local Similarity 35.2%; Pred. No. 4.3e-48;
 Matches 198; Conservative 87; Mismatches 220; Indels 57; Gaps 17;

Qy	68	LYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKH-KDECHNFIKVLK	126
		: : : : : : : :	
Db	69	LYVGAKDHIFSFL-----VNIKEYQKIVWPVSHSRDECKWAGKDILRECANFIKVLKT	123
Qy	127	KNDDALFVCGTNAFNPSCR-----NYKMDTLEPFGDEF--SGMARCPYDAKHANVALFAD	179
		: : : : : : :	
Db	124	YNQTHLYACGTGAFHPMCTYIEVGSHPEDNIFRMEDSHFENGGRGKSPYDPKLLTASLLVD	183
Qy	180	GKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYI	232
		: : : : : : : : :	
Db	184	GELYSGTAADFMRDFAIFRTLGHHPHPIRTEQHDSRWLNDPRFISAHLPESDNPEDDKI	243
Qy	233	YFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPG----D	288
		: : : : : : : :	
Db	244	YFFFRENAIDGEHTGKATHARIGQICKNDFGG-HRSLVNKWTTFKLKARLICSVPGPNGID	302
Qy	289	SHFYFNILQAVTDVIRINGRD-----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFK	344
		: : : : : : : :	
Db	303	THF-----DELQDVFLMNSKDPKNPIVYGVFTTSSNIFKGSAVCMYSMTDVRVFLGPYA	357
Qy	345	EQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPS	404
		: : : : : : : : :	
Db	358	HRDGPNYQWVPY-QGRVPYPRPGTCP-SKTFGGFDSTKDLPEDEVITFARSHPAMYNPVFP	415
Qy	405	IFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL	464
		: : : : : : : : : : : :	
Db	416	INSRPIMIKTDVDYQFTQIVVDRVDAEDGQYDVMFIGTDIGTVLKVVSIPKETWHELEEV	475
Qy	465	FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKT	524
		: : : : : : : : :	
Db	476	LLEEMTVFR-----EPTVISAMKISTKQQQLYIGSATGVSQPLHRCDVYGKACAE	526
Qy	525	CIASRPYCGWIKEGGACSHLSPNS-RLTFEQDIERGNTDGLGDCHNSFVALNGHSSSL	583
		: : : : : :	
Db	527	CCLARDPYCAW--DGSSCSRYFPTAKRRTRRQDIRNG--DPLTHCSD---LQHHDN---	575

Qy 584 PSTTTSDSTAQEGYESRGGMLD 605
|| | : | | : | :
Db 576 PSGQTLEEKIIYGVENSSTFLE 597

RESULT 7

JC5928

semaphorin F precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 17-Nov-2000

C;Accession: JC5928

R;Simmons, A.D.; Pueschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.
Biochem. Biophys. Res. Commun. 242, 685-691, 1998

A;Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-
chat candidate interval.

A;Reference number: JC5928; MUID:98125554; PMID:9464278

A;Accession: JC5928

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1074 <SIM>

A;Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584

A;Experimental source: brain

C;Comment: This protein disrupts normal brain development and leads to some of
the features of Cri-du-chat.

C;Genetics:

A;Gene: semaF

C;Superfamily: human semaphorin F; thrombospondin type 1 repeat homology

F;1-20/Domain: signal sequence #status predicted <SIG>

F;50-533/Domain: semaphorin #status predicted <SEM>

F;840-896/Domain: thrombospondin type 1 repeat homology <THR3>

F;971-993/Domain: transmembrane #status predicted <TMM>

Query Match 15.2%; Score 830; DB 2; Length 1074;
Best Local Similarity 36.2%; Pred. No. 3.1e-47;
Matches 199; Conservative 90; Mismatches 211; Indels 50; Gaps 17;

Qy 68 LYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKK 127
| : ||::: : : |:: : : | : :| | || |::|| |::|||
Db 70 LVVGARNYLFRLQL-----EDLSLIQAVEWECDEATKKACYSKKGSKKEECQNYIRVLL-V 123

Qy 128 NDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF-ADGKLYSAT 186
| || ||||| || | : | | : ||||| : | : || | |::|||
Db 124 GGDRLFTCGTNAFTPVCTNRSLSNLAEIHDQISGMARCPYSPQHNSTALLTAGGELYAAT 183

Qy 187 VTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTM 246
|| | ||||| | ||| ::||| || | : | |:: ||||| ||:::
Db 184 AMDFPGRDPAIYRSLGILPPLRTAQYNSKWLNEPNFVSSYDIGNFTYFFFRENAVEHD-C 242

Qy 247 GKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSPVGD SHFYFNILQAVTDVIRIN 306
|| || | |::|||::|| : :|| ||::||| ||| ||: ||:| ||: : :
Db 243 GKTVFSRAARVCKNDIGG-RFLL EDTWTTFMKARLNC SRPGEVPFYYNELQSTFFLP EL- 300

Qy 307 GRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRP 366
|:: |::| ||| |||| ::| || |:: || |:: | | | |:
Db 301 --DLIYGIFTTNVNSIAASAVCVFNLSAIAQAFSGPFPKYQENSRS AWLPYPN---PNPHF 355

Qy	367	GCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVD	426
Db	356	QCGTVDQGLYVNLTERNL-QDAQKFILVH----EVVQPVTTPVPSFMEDNSRF--SHVAVD	408
Qy	427	TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKR	486
Db	409	VVQGREALVHIIYLATDYGTIKKVRVPLNQT---SSSCLLEEIELPERR-----REP	458
Qy	487	IMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGGACSHLS	546
Db	459	IRSLQILHSQSVLFVGLREHVVKIPLKRCQFY-RTRST'CIGAQDPYCGWDVVMKKCTSLE	517
Qy	547	PNSRLT-FEQDIERGNTDGLGDCHNSFVALNGHSSSLLPST--TTSDSTAQEGYESRGGM	603
Db	518	ESLSMTQWEQSISA-----CPTRNLTVDGHFGVWSPWTPCTHTDGSAV-----GSC	563
Qy	604	LDWKHLLDSP	613
Db	564	LCRTRSCDSP	573

Qy	66	GTLYIAARDHIYTVDDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKH-KDECHNFIKVL	124
		: : : : : : : : : : :	
Db	65	GRLFGVAENHVASLNLDNISKR---AKKLAWPAPVEWREECNWAGKDIGTECMNFVKLL	120
Qy	125	LKKNDDALFVCGTNAFNPSCRNYKMD-----TLEPFGDEFSGMARCPYDAKHANVAL	176
		: : : : : : : :	
Db	121	HAYNRTHLLACGTGAHFPTCAFEVGVHRAEEPVLRLDP-GRIEDGKGKSPYDPRHRAASV	179
Qy	177	FADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFQAV-----DYG	229
		: : : : : : : :	
Db	180	LVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWLNPEKFKVFWIPESENPDD	239
Qy	230	DYIYFFFREIAVE-YNTMGKVVFPFRAQVCKNDMGGSQVRLEKQWTSFLKARLNCVSP--	286
		: : : : : : : :	
Db	240	DKIYFFFRETAVEAAPALGRLSVSRVGOICRNDVGG-ORSLVNKWTTFCLKARLVCSVPGV	298

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Qy      287 -GDSHFYFNILQAVTDVIRINGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTG 341
      ||:||      : ||  :: ||      :: | ||| :  |||| | | :  | |
Db      299 EGDTHF-----DQLQDVFLLSRDHRTPLLYAVFSTSSSIFQGSAVCVYSMNDVRRRAFLG 353

Qy      342 RFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEA 401
      |  :: |  |      ||| |||| |  | :  :::: :||| :  | : ||| :
Db      354 PFAHKEGPMHQWVSQY-QGRVPYPRPGMCP-SKTFTGTFSSSTKDFPDDVIQFARNHPLMYS 411

Qy      402 VPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN 461
      |      || ||:  |  |:|| |  |  :: |:||:: | :|| ::  |
Db      412 VLPTGGRPLFLQVGANYTFTQIAADRVAAADGHYDVLFIGTDVGTVLKVISVPKGSRPSA 471

Qy      462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRRCERHGKC 521
      : | ||| : | :      :  : ||:  ||| : | :: | || ||:
Db      472 EGLLLEELHVFE-----DSAAVTSMQISSKRHQLYVASRSAVAQIALHRCAAHGRV 522

Qy      522 KKTCIASRDYPYCGWIKGACSHLSPNSRLTF-EQDIERGNTDGLGDCHNSFVALNGH-- 578
      |  :||| |  :| ||:  |::: |  ||: | :  |  :| || |
Db      523 CTECCCLARDPYCAW--DGVACTRFQPSAKRRFRQDVRNGDPSTLCSGDSSRPALLEHKV 580

Qy      579 -----SSSLPSTTTSDSTAQEGYESRGGM 603
      ||: |  |  |  |  ||:
Db      581 FGVEGSSAFLECEPRSLQARVEWTFQAGV 610

```

RESULT 9

I48744

semaphorin A - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C;Accession: I48744

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48744

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-748 <RES>

A;Cross-references: EMBL:X85990; NID:g854323; PIDN:CAA59982.1; PID:g854324

C;Genetics:

A;Gene: semA

C;Superfamily: semaphorin

```

Query Match          14.7%; Score 803; DB 2; Length 748;
Best Local Similarity 35.5%; Pred. No. 1.1e-45;
Matches 191; Conservative 80; Mismatches 205; Indels 62; Gaps 18;

```

```

Qy      66 GTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKH-KDECHNFIKVL 124
      | |:: | :::: |      :||| | :  : |  ||  || ||:::|
Db      65 GRLFVGAENHVASLSLDNISKR----AKKLAWPAPVEWREECNWAGKDIGTECMNFVRL 120

Qy      125 LKKND DALFVCGTNAFNPSCRNYKMDTL-----EPFGDEFSGMARCPYDAKHANVA 175
      |  |  | | ||::| :  |  |  |  | : ||| :|  :
Db      121 HAYNHTLLACRTGAFHPTCALWRWATAGGTHASTGPEKLED---GKGKTPYDPRHRPPS 177

```

Qy	176	LFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAV-----DY	228
		: : : : :: : : :	
Db	178	VLVGEELYSGVTADLMGRDFTIFRSLGQNPSLRTEPHDSRWLNPKFVKVFWIPESENPD	237
Qy	229	GDYIYFFFFREIAVE-YNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVP-	286
		:: : : : : : :	
Db	238	DDKIYFFFRESAVEAAPAMGRMSVSRVQGICRNDLGG-QRSLVNKWTTFCLKARLVCSVPG	296
Qy	287	--GDSHFYFNILQAVTDVIRINGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFT	340
		: : : : : : :	
Db	297	VEGDTHF-----DQLQDVFLSSRDQTPLLYAVFSTSSGVFQGSAVCVYSMNDVRR AFL	351
Qy	341	GRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDE	400
		: : : : : : : :	
Db	352	GPLPHKEGPTHQWVSY-QGRVPYPRPGMCP-SKTFGTFSSTKDFPDDVIQFGRNHPLMYN	409
Qy	401	AVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLA----RIGN	456
		: : : : : : : : : : :	
Db	410	PVLPMGGRPLFLQVGAGYTFTQIAADRVAADGHYDVLFIGTDVGTVLKVISVPKGRPN	469
Qy	457	SGFLNDSLFLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCE	516
		: : : : : : :	
Db	470	S----EGLLLEELQVFE-----DSAAITSMQISSKRQQLYVASRAAVAQIALHRCT	516
Qy	517	RHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTF-EQDIERGNTDGL--GDCHNS	571
		: : : : : : :	
Db	517	ALGRACAECCLARDPYCAW--DGSACTRFQPTAKRRERRODIRNGDPSTLCSGDSSHS	572

Qy	169	AKHANVALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA---	225
Db	67	PKLLTASLLIDGELYSGTAANFMGRDFAIFRTLGHHPHPIRTEQHDNRWLNDPRFISAHLI	126
Qy	226	----VDYGDYIYFFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQVRLEKQWTSFLKARL	281
Db	127	PESDNPEDDKVYFFFFRENAIDGEHSGKATHARIGQICKNDFGG-HRSLVNKWTTFCLKARL	185
Qy	282	NCSVPG----DSHFYFNILQAVTDVIRINGRD----VVLATFSTPYNSIPGSAVCAYDML	333
Db	186	ICSVPGPNGIDTHF-----DELQDVFLMNSKDPKNPIVYGVFTTSSNIFKGSAVCMYSMS	240
Qy	334	DIASVFTGRFKEQKSPDSTWTPVPDERVPPKPRGCCAGSSSLERYATSNEFPDDTLNFIK	393
Db	241	DVRRVLLGPYAHRDGPNYQWVPY-QGRVPYPRPGTCP-SKTFGGFDSTKDLPPDDVITFAR	298
Qy	394	THPLMDEAVPSIFNRPWFRLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLAR	453
Db	299	SHPAMYNPVFPINNRPIMIKTDVNYQFTQIVVDRDAEDGQYDVMFIGTVDGTVLKVVS	358
Qy	454	IGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLG	513
Db	359	PKETWHDLLEEVLEEMTVFR-----EPTTISAMELSTKQQQLYIGSTAGVAQLPLH	409
Qy	514	RCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNS-RLTFEQDIERGNTDGLGDCHNSF	572
Db	410	RCDIYGKACAECCCLARDPYCAW--DGSSCSRYFPTAKRRTRRQDIRNG--DPLTHCSDLQ	465
Qy	573	VALNGHSSSL----LPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQ	628
Db	466	HHDNHHGPSLEERIYGVENSSTFLECSPKSQRALVYWQFQRNEDRKEEI-KMGDHIIR	524
Qy	629	DKKGVIRESYLK	640
Db	525	TEQGLLLRLSLQK	536

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A;Map position: 1
```


A; Introns: 36/1; 70/2; 85/3; 194/2; 221/1; 253/3; 301/1; 352/3; 522/2; 560/1; 599/3; 655/3

Query Match 14.5%; Score 789; DB 2; Length 712;
Best Local Similarity 28.7%; Pred. No. 9.1e-45;
Matches 229; Conservative 129; Mismatches 282; Indels 158; Gaps 29;

```
Qy      6 LLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYP-----VFVGHKPGRNNTQQRHRLDIQ 59
      ||| | ::          || | : |          | : | : | |          |
Db      7 LLLLFNVV-----RSSEAIT---GGVVNLRPKQIINSVGIGDRFGGIGTSSDESDFH 55

Qy     60 MIMIMNG-TLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECH 118
      :: :| :| : ||: :| : : |          : : | : ||          :: | |||| | :|
Db     56 KLLAADGDSLLVGARNAVYNLSLST-----LSVNHKIDWKPPAEHIEECIMKGKSKTDCQ 110

Qy    119 NFIKVLKKND DALFVCGTNAFNPSCRNYKMDTLEPGF----DEFSGMARCPYDAKHANV 174
      |:|:| | :|:      |||:|:| | | | | | : | |          :| |          ||| | | :
Db    111 NYIRVLARKSAGVSLVCGTHAFSPKCREY---TVTEFGIRNTRQFDGQGISEPYDPKHNS 167

Qy    175 ALFADG--KLYSATVTDFLAIDAVIYR-SLGESPT-----LRTVKHDSKWLKEPYFVQA 225
      ||: | :|: |||||: ||:| | :|:| :|:| :|| :|:| | | | |
Db    168 ALYVPGTNQLFVATVTDFVGN DALIYRKTIDETPSSKSAANIRTQSYDARVLNAPNFVAT 227

Qy    226 VDYGDYIYFFFREIAVEY--NTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNC 283
      | ::|:|:| | | | | | :| :| :|:| | | | | | | | :| :|:|:| | | | |
Db    228 FAYKEHVYFWFREIASEAIDNNEEPQIYARVARVCKNDKGA-RPANERWTSYKARLNC 286

Qy    284 SVP-GDSHFYFNILQAVTDVIRI-NGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVF-T 340
      |:| | | | | | | :|:| | | | | | | | | | : : | | | : | | | |
Db    287 SLPSSGSSPFYFNELKAVSDPIDAGNNNHVVYTVFSTPDS DVRMSAVCKFMSKKIREFDN 346

Qy    341 GRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDE 400
      | | | | : | | | | | | | | : | :          : |:|:|:| | | | :
Db    347 GTFKHQNNAQSMWMAFNREVPKPRPGSCSPDST-----KLPENTVSFILHHP LHR 398

Qy    401 AVPSIFNRPWFLRMTVRYRLTKIAV---DTAAGPYQNHTVVFLGSEKGIILKFLARIGNS 457
      :|:| : | : | | | :| | | | : | : :|:|:| : | :| : | | :
Db    399 PIPSV-AAPLLVEGADRADLTQITVLPVRVAVGGH-NYDILFIGTSDGKVLKVVEVDGNA 456

Qy    458 GFLND-SLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCE 516
      : :| : : |          |          | : : : : :|: |
Db    457 TVIQSATVFQRGVPIVN-----LLTTKESVVIVSADEIASLPVHNCA 498

Qy    517 RHGKCKKTCIASRDPYCGWIKGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN 576
      : | | | : :|:| | | | | | : | | : | :|:| : | : | :
Db    499 QQTSCSK-CVQLQDPHCAWDSSIARCVHGGSWTGDQFIQNMVFGQSE---QCPEGIIV-- 552

Qy    577 GHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHL LDPDSTDPLGAVSSHNH QDKKGVIRE 636
      : : | :| | | | | | | |
Db    553 -----REVFDNESEAQPEAVS-----RS 571

Qy    637 SYLKGH DQLVPVTL LAIVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHS-- 694
      | | | : | : |:| : : :| | | | | : | : | : |
Db    572 GYPKEHSTITVVLVAASLISLIIGA-FIGIRV-----NRWAATSEPHRSASSTSGSDY 625

Qy    695 -----RRGSMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKA 745
      | |:|: ||: |          : | : : | | |
```


Qy 352 TWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRP-W 410
 | | : | | : | | | | : | | | | : | | : | | :
 Db 382 AWLPVLNSRVPEPRPGTCVNDTS-----NLPDVLNFIKTHPLMDKAVNHEHNNPVY 433

Qy 411 FLRTMVRYRLT--KIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEE 468
 : | : | : | | : | : | : | | : | : | : | : |
 Db 434 YKRDVFTKLVDKIRIDIL---NQEYIVYVGTNLGRIYKIVQYYRNGESLSKLLDIFE 490

Qy 469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC-ERHGKCKKTCIA 527
 :: : : | | : : | | : : | | : : | : | :
 Db 491 VA-----PNEAIQVMEISQTRKSLYIGTDHRIKQIDLAMCNRRYDNCFR-CV- 536

Qy 528 SRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTD 563
 | | | | | | | | | | : | | : | :
 Db 537 -RDPYCGWDKEANTCRPY----ELDLLQDVANETSD 567

RESULT 13

G02173

semaphorin III family homolog - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999

C;Accession: G02173

R;Naylor, S.

submitted to the EMBL Data Library, October 1995

A;Reference number: G09275

A;Accession: G02173

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-753 <NAY>

A;Cross-references: EMBL:U38276; NID:g1061350; PIDN:AAB18276.1; PID:g1061351

C;Superfamily: semaphorin

Query Match 14.1%; Score 768; DB 2; Length 753;
 Best Local Similarity 31.6%; Pred. No. 2.5e-43;
 Matches 191; Conservative 109; Mismatches 207; Indels 98; Gaps 22;

Qy 6 LLLYFTLLHFAGAGFPEDSEPISSHGNKYKQYPVFVGHKPGRNTTQRHRLDIQMI---- 61
 | | : | | : | | | | : | | : | | : | :
 Db 6 LLLWASLLTGAWPSFPTQD-----HLP---ATPRVRLSFKELKATG 43

Qy 62 -----MIMNGT-----LYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQA 102
 : : | | : : : : : : : : : : : : : :
 Db 44 TAHFFNLLNTTDYRILLKDEDHDMYVGSKDYLVDLHDINREPLI----IHWAASPQ 99

Qy 103 DVDTCRMKGKH-KDECHNFIKVLKKNDDALFVCGTNAFNPS-----RNYKMDTL 152
 : : | : | | | | : : : : | : | | | : : : : :
 Db 100 RIEECVLSGKDVNGECGNFVRLIQPNRTHLYVCGTGAYNPMCTYVNRGRRAQDY-IFYL 158

Qy 153 EPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRVTKH 212
 | | | | : | | : : : : : : : : : : : : : :
 Db 159 EPERLE-SGKGKCPYDPKLDTASALINEELYAGVYIDFMGTDAAFRTLKGQTAMRTDQY 217

Qy 213 DSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQ 266
 : : | : | : | : : : | : | | | : : : : : : :
 Db 218 NSRWLNDPFSFIHAELIPDSAENDDKLYFFFRERSAE-APQSPAVYARIGRICLNDDGGHC 276

Qy 267 RVLEKQWTSFLKARLNCSVPGDS--HFYFNILQAV----TDVIRINGRDVVLATFSTPYN 320
 :: | |::| | | | | | | | | | : : | | | | : | : | | : :
 Db 277 CLVNK-WSTFLKARLVCSVPGEDGIETHFDELQDVFVQQTQDVR---NPVIYAVFTSSGS 332
 Qy 321 SIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVVKPRPGCCAGSSSLERYAT 380
 | | | | | | | | | | | | : : | : | | : : | | | | | : :
 Db 333 VFRGSAVCVYSMADIRMVFNPGFAHKEGPNYQWMPF-SGKMPYPRPGTCPPGGTFTPSMKS 391
 Qy 381 SNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA--VDTAAGPYQNHTV 437
 : : | | : : | | : : | | : | : | | | | | | | | | : |
 Db 392 TKDYPDEVINFMRSHPLMYQAVYPLQRRPLVVRTGAPYRLTTIAVDQVDSADGRYE---V 448
 Qy 438 VFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASS 497
 : | | : : | : | : : : | | | : | : : : | : :
 Db 449 LFLGTDGRGTQKVIV-LPKDDQEMEELMLEEVEVFK-----DPAPVKMTMTISSKRQ 498
 Qy 498 SLYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNS-RLTFEQD 556
 | | | : | : | | : : | : | | | | : | | | : : | | : | |
 Db 499 QLYVASAVGVTHLSLHRCQAYGAACADCCCLARDPYCAW--DQACSRYTASSKRRSRRQD 556
 Qy 557 IERGN 561
 : | |
 Db 557 VRHGN 561

RESULT 14

I48748

semaphorin E - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C;Accession: I48748

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48748

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-751 <RES>

A;Cross-references: EMBL:X85994; NID:g854331; PIDN:CAA59986.1; PID:g854332

C;Genetics:

A;Gene: semE

C;Superfamily: semaphorin

Query Match 13.5%; Score 737; DB 2; Length 751;

Best Local Similarity 31.3%; Pred. No. 3e-41;

Matches 187; Conservative 103; Mismatches 234; Indels 74; Gaps 18;

Qy 24 SEPISISHGNYTKQYPVFVGHKPGRNTTQHRRLDIQMIMI--MNGTLYIAARDHIYTVDI 81
 | | | : | | : | | : : : : : : : : : | : : | : : | : : |
 Db 42 SEYFSLSH-----QQLDYRILLMDEDQDRIYVGSKDHLISLNI 79
 Qy 82 DTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDE-CHNFIKVLLKKNDDALFVCGTNAF 140
 : | : : | : | : | : | | | | : : : : | | : | : | : | : |
 Db 80 NNISQEPL----SVFWPASTIKVEECKMAGKDPHGCQGNFVRVIQTFNRTHLYVCGSGAF 135

QY 141 NPSC----RNYKMDTLEPFGDEF-----SGMARCPYDAKHANVALFADGKLYSATVT 188
 :| | : : | : || || : : : :|
 Db 136 SPVCTYLNRGRSE-----DQVFMIDSKCESGKGRCSEFNPVNVTVSVMINEELFSGMYI 189

QY 189 DFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGD-YIYFFFREIAV 241
 ||: || |:|| : ||| :|:|||| || || | | :|:|:|
 Db 190 DFMGTDAAIFRSLTKRMLRTDQHNSKWLSEPMFVDAHVIPDGTDPNDAKVYFFFKERLT 249

QY 242 EYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDS--HFYFNILQAV 299
 : | : :|:| || || || :|:|:| || | : :|:| : |
 Db 250 DNNRSTKQIHSMIARICPNDTGG-QRSLVNKWTTFKARLVCSVTDEDGPETHFDELEDV 308

QY 300 TDVIRINGR-DVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPD 358
 : | | :| |:| : |||| | : || :| | | : :| :
 Db 309 FLLETDNPRRTLVIYGIFTTSSSVFKGSAVCVYHLSDIQTVFNGPFAHKEGPNHQLISY-Q 367

QY 359 ERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRY 418
 |:| |||| | : | :|:| : ||: |||| : : | || :| |
 Db 368 GRIPYPRPGTCPGGAFTPNMRTTKDFPDDVVTFIRNHPLMYNSISPIHRRPLIVRIGTDY 427

QY 419 RLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCS 478
 : ||||| : |:|:|:| : | : || : | ||| : : :
 Db 428 KYTKIAVDRVNAADGRYHVLFLGTDRTGVQKVVLPTNSS-ASGELILEELEVFKNH--- 483

QY 479 YDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKE 538
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 Db 484 -----VPITTEISSKKQQLYVSSNEGVSQVSLHRCHIYGTACADCCCLARDPYCAW--D 535

QY 539 GGACSHLSP-NSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQE 595
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 Db 536 GHSCSRFYPTGKRRSRQDVRHGNP--LTQCRGFNLKAYRNAAEIVQYGVRRNNSTFLE 591

RESULT 15

S66498

M-sema F protein precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 24-Nov-1999

C;Accession: S66498

R;Inagaki, S.; Furuyama, T.; Iwahashi, Y.

FEBS Lett. 370, 269-272, 1995

A;Title: Identification of a member of mouse semaphorin family.

A;Reference number: S66498; MUID:95385809; PMID:7656991

A;Accession: S66498

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-834 <INA>

A;Cross-references: EMBL:S79463; NID:g1110598; PIDN:AAB35184.1; PID:g1110599

C;Superfamily: semaphorin

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-834/Product: M-sema F protein #status predicted <MAT>

Query Match 12.7%; Score 692; DB 2; Length 834;

Best Local Similarity 26.0%; Pred. No. 3.7e-38;

Matches 232; Conservative 131; Mismatches 326; Indels 204; Gaps 34;

QY 65 NGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGK-HKDECHNFIKV 123

Db	62	SGLLYVGAREALFAFSV-----EALELQGAISWEAPAEKKIECTQKGKSNQTECFNFIRF	116
Qy	124	LLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEF-SGMARCPYDAKHANVALFADGKL	182
Db	117	LQPYNSSHLVCGTYAFQPKCTYINMLTFTLDRAEFEDGKGKCPYDPAKGHTGLLDVGEL	176
Qy	183	YSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYI	232
Db	177	YSATLNNFLGTPEVILRYMGTHHSIKT-EYLAFWLNEPHFVGSAFVPESVGSFTGDDDKI	235
Qy	233	YFFFREIAVEYNTMGKVVFPRAVQCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFY	292
Db	236	YFFFSERAVEYDCYSEQVVARVARVCKGDMGGA-RTLQKKWTTFLKARLVCSAP-DWKVY	293
Qy	293	FNILQAVTDVIRINGRDVV-LATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDS	351
Db	294	FNQLKAVHTLRGASWHNTTFFGVFQARWGDMDLSAVCEYQLEQIQQVFEGPYKEYSEQAQ	353
Qy	352	TWTPVPDERVPKPRPGCCAGSSSLER-YATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW	410
Db	354	KWARYTDP-VSPRPGSCINNWHRDNGYTSSLELPDNTLNFIKKHPLMEDQVKPRLGRPL	412
Qy	411	FLRTMVRYLTKIAVDTAAG-PYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL-----	464
Db	413	LVKKNTNF--THVVADRVPLDGATYTVLFIGTGDGWLLKAV-----SLGPWIH	459
Qy	465	FLEEMSVYNSEKCSYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKT	524
Db	460	MVEELQVFDQEP-----VESLVLSSQSKVLFAGSRSQVLQSLADCTKYRFC-VD	508
Qy	525	CIASRPYCGWIKEGGAC-----SHLS--PNSRLTFEQDIER-----	559
Db	509	CVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYGIKKVRSIPKNITV	568
Qy	560	-GNTDGLGDCHNSFVALNGH---SSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDS	615
Db	569	VSGTDLVLPCHLSSNLAHAHWTFGSQDLPAEQPGSFLYDTGLQALVVM-----	616
Qy	616	TDPLGAVSSH-----HQDKKG--VIRESYLKG-----HDQLVPVTL LAI AVILAFV	660
Db	617	----AAQSRHSGPYRCYSEEQGTRLAAESYLVAVVAGSSVTLEARAPLENLGLVWLAVVA	672
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKL SGLFGDTQSKDPKPE	720
Db	673	LGAVCL-VLLLLVLSLRRR-----LREELE-----KGAKAS-----ER	704
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREW---	777
Db	705	TLVYPL-----ELPKEPASPPF--RPGPETDEKLWDPV	735
Qy	778	-----ERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQ	832
Db	736	GYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLPS--PTRLHLGGGRNSNANGYVR-	792
Qy	833	PKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQRE	885

Db 793 -----LQLGGEDRGGS-----GHPLPELADELRRKLQQRQ 822

Search completed: March 24, 2004, 13:17:10
Job time : 33.8439 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:14:29 ; Search time 74.7731 Seconds
(without alignments)
3567.110 Million cell updates/sec

Title: US-09-856-681A-2
Perfect score: 5450
Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						

1	5450	100.0	1030	12	US-10-016-248-63	Sequence 63, Appl
2	5431.5	99.7	1047	12	US-10-403-676-48	Sequence 48, Appl
3	5431.5	99.7	1047	15	US-10-449-548-48	Sequence 48, Appl
4	5422.5	99.5	1047	10	US-09-957-187-85	Sequence 85, Appl
5	5422.5	99.5	1047	12	US-10-403-676-14	Sequence 14, Appl
6	5422.5	99.5	1047	15	US-10-449-548-14	Sequence 14, Appl
7	5368	98.5	1018	12	US-10-403-676-28	Sequence 28, Appl
8	5368	98.5	1018	15	US-10-449-548-28	Sequence 28, Appl
9	5349.5	98.2	1035	12	US-10-403-676-18	Sequence 18, Appl
10	5349.5	98.2	1035	15	US-10-449-548-18	Sequence 18, Appl
11	5134.5	94.2	998	12	US-10-403-676-20	Sequence 20, Appl
12	5134.5	94.2	998	15	US-10-449-548-20	Sequence 20, Appl
13	5113.5	93.8	981	12	US-10-403-676-30	Sequence 30, Appl
14	5113.5	93.8	981	15	US-10-449-548-30	Sequence 30, Appl
15	5109.5	93.8	971	12	US-10-403-676-46	Sequence 46, Appl
16	5109.5	93.8	971	15	US-10-449-548-46	Sequence 46, Appl
17	4921	90.3	939	10	US-09-957-187-4	Sequence 4, Appli
18	4921	90.3	939	12	US-10-403-676-32	Sequence 32, Appl
19	4921	90.3	939	15	US-10-449-548-32	Sequence 32, Appl
20	4590.5	84.2	884	10	US-09-957-187-6	Sequence 6, Appli
21	4346.5	79.8	888	12	US-10-016-248-64	Sequence 64, Appl
22	3373	61.9	630	10	US-09-957-187-30	Sequence 30, Appl
23	3368	61.8	861	12	US-10-403-676-52	Sequence 52, Appl
24	3368	61.8	861	15	US-10-449-548-52	Sequence 52, Appl
25	3367.5	61.8	636	12	US-10-403-676-36	Sequence 36, Appl
26	3367.5	61.8	636	15	US-10-449-548-36	Sequence 36, Appl
27	3363	61.7	666	12	US-10-403-676-56	Sequence 56, Appl
28	3363	61.7	666	15	US-10-449-548-56	Sequence 56, Appl
29	3362	61.7	626	10	US-09-957-187-83	Sequence 83, Appl
30	3362	61.7	626	12	US-10-403-676-34	Sequence 34, Appl
31	3362	61.7	626	15	US-10-449-548-34	Sequence 34, Appl
32	3351.5	61.5	649	12	US-10-403-676-50	Sequence 50, Appl
33	3351.5	61.5	649	15	US-10-449-548-50	Sequence 50, Appl
34	3349.5	61.5	878	12	US-10-403-676-54	Sequence 54, Appl
35	3349.5	61.5	878	15	US-10-449-548-54	Sequence 54, Appl
36	3285.5	60.3	640	12	US-10-403-676-16	Sequence 16, Appl
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38	2627	48.2	497	12	US-10-403-676-24	Sequence 24, Appl
39	2627	48.2	497	15	US-10-449-548-24	Sequence 24, Appl
40	2545	46.7	479	12	US-10-403-676-26	Sequence 26, Appl
41	2545	46.7	479	15	US-10-449-548-26	Sequence 26, Appl
42	2349.5	43.1	1088	12	US-10-016-248-20	Sequence 20, Appl
43	2335	42.8	1035	12	US-10-016-248-12	Sequence 12, Appl
44	2330	42.8	442	12	US-10-403-676-22	Sequence 22, Appl
45	2330	42.8	442	15	US-10-449-548-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
 US-10-016-248-63
 ; Sequence 63, Application US/10016248
 ; Publication No. US20040033491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsobrook et al.

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; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 1030
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-63

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Query Match          100.0%; Score 5450; DB 12; Length 1030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 60

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Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGWIKEGG 540
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Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
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RESULT 2

US-10-403-676-48

; Sequence 48, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 48
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-48

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Best Local Similarity 98.4%; Pred. No. 0;
Matches 1030; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

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Db	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRVVKHDSKWKEPYFVQAVDYGDIYFFFREIA	240
Db	181	KLYSATVTDFLAIDAVIYRSLGESPTLRVVKHDSKWKEPYFVQAVDYGDIYFFFREIA	240
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Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG	540
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSL	583
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSL	600
Qy	584	PSTTTSDSTAQEGYESRGGMLDWKHL L DSDPDSTPLGAVSSH NHQDKKGVIRESYLK GHD	643
Db	601	PSTTTSDSTAQEGYESRGGMLDWKHL L DSDPDSTPLGAVSSH NHQDKKGVIRESYLK GHD	660
Qy	644	QLVPV TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	703
Db	661	QLVPV TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	720
Qy	704	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	763
Db	721	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	780
Qy	764	LQQKRKPSRGSREWERNQN LINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVL PITQQ	823

Db	781		LQQKRKPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQ	840
Qy	824		GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	883
Db	841		GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	900
Qy	884		REASLGPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNTNSSN	943
Db	901		REASLGPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNTNSSN	960
Qy	944		SSHLSRNQSFGRGDNPPAPQVRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961		SSHLSRNQSFGRGDNPPAPQVRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
Qy	1004		PSLKPDPVPPKPSFAPLSTSMKPNDACT	1030
Db	1021		PSLKPDPVPPKPSFAPLSTSMKPNDACT	1047

RESULT 3

US-10-449-548-48

; Sequence 48, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRochelle, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 60/234,082

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: 60/233,798

; PRIOR FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: 60/174,485

; PRIOR FILING DATE: 2000-01-04

; PRIOR APPLICATION NUMBER: 10/403,676

; PRIOR FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/384,798

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: 60/402,407

; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 48
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-48

Query Match 99.7%; Score 5431.5; DB 15; Length 1047;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1030; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
        |||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120
        |||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120

Qy    121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
        |||
Db    121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
        |||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVT 300
        |||
Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
        |||
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
        |||
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 480
        |||
Db    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 480

Qy    481 GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGWKEGG 540
        |||
Db    481 GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGWKEGG 540

Qy    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSSL 583
        |||
Db    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSSL 600

Qy    584 PSTTTSDSTAQEGYESRGGMLDWKHL LDDSPDSTDPLGAVSSH NHQDKKGVIRESYLK GHD 643
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; ORGANISM: Homo sapiens
US-09-957-187-85

Query Match 99.5%; Score 5422.5; DB 10; Length 1047;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1029; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHCNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120

Qy    121 IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEKPYFVQAVDYGDIYFFFREIA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEKPYFVQAVDYGDIYFFFREIA 240

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480

Qy    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGG 540

Qy    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSLL 583
        ||||||||||||||||||||||||||||||||||||||||||||
Db    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSLL 600

Qy    584 PSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGH 643
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 PSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGH 660

Qy    644 QLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT 703
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 QLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT 720

Qy    704 KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPT 763
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db	721	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPT	780
Qy	764	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQ	823
Db	781	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQ	840
Qy	824	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVLNLDLPPKVPQ	883
Db	841	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVLNLDLPPKVPQ	900
Qy	884	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRNTNSSN	943
Db	901	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRNTNSSN	960
Qy	944	SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961	SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
Qy	1004	PSLKPDPVPPKPSFAPLSTSMKPNDACT	1030
Db	1021	PSLKPDPVPPKPSFAPLSTSMKPNDACT	1047

RESULT 5

US-10-403-676-14

; Sequence 14, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.

```

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 14
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-14

```

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Query Match          99.5%; Score 5422.5; DB 12; Length 1047;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1029; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
        |||||||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SHCNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
        |||||||

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS RQADVDTCRMKGKHKDECHNF 120
        |||||||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS RQADVDTCRMKGKHKDECHNF 120
        |||||||

Qy    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
        |||||||
Db    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
        |||||||

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
        |||||||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
        |||||||

Qy    241 VEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
        |||||||
Db    241 VEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
        |||||||

```

Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWIKGG	540
Db	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWIKGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSLL	583
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSLL	600
Qy	584	PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSSHNHQDKKGVIRESYLKGH	643
Db	601	PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSSHNHQDKKGVIRESYLKGH	660
Qy	644	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	703
Db	661	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	720
Qy	704	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPT	763
Db	721	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPT	780
Qy	764	LQQRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQ	823
Db	781	LQQRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQ	840
Qy	824	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGMVNLVENLDSLPPKVPQ	883
Db	841	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGMVNLVENLDSLPPKVPQ	900
Qy	884	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTILKRNNNTSSN	943
Db	901	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTILKRNNNTSSN	960
Qy	944	SSHLSRNQSFGRGNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961	SSHLSRNQSFGRGNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
Qy	1004	PSLKPDVPPKPSFAPLSTSMKPNDACT	1030
Db	1021	PSLKPDVPPKPSFAPLSTSMKPNDACT	1047

RESULT 6

US-10-449-548-14

; Sequence 14, Application US/10449548

```

; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 14
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-14

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Query Match          99.5%; Score 5422.5; DB 15; Length 1047;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1029; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
        |||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHCNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120
        |||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120

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Qy	121	IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Db	121	IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEKPYFVQAVDYGDIYFFFREIA	240
Db	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEKPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG	540
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSL	583
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSL	600
Qy	584	PSTTTSDSTAQEGYESRGGMLDWKHLSDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGH	643
Db	601	PSTTTSDSTAQEGYESRGGMLDWKHLSDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGH	660
Qy	644	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT	703
Db	661	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT	720
Qy	704	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	763
Db	721	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	780
Qy	764	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI	823
Db	781	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI	840
Qy	824	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	883
Db	841	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	900
Qy	884	REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTSSN	943
Db	901	REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTSSN	960
Qy	944	SSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003

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          |||||||
Db      961 SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT 1020

Qy      1004 PSLKPDVPPKPSFAPLSTSMKPNDACT 1030
          |||||||
Db      1021 PSLKPDVPPKPSFAPLSTSMKPNDACT 1047

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RESULT 7

US-10-403-676-28

; Sequence 28, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: LaRochelle, William J.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Li, Li

; APPLICANT: Liu, Xiaohong

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Millet, Isabelle

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Patturajan, Meera

; APPLICANT: Peyman, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Reiger, Daniel

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE

; FILE REFERENCE: 21402-573B

; CURRENT APPLICATION NUMBER: US/10/403,676

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 09/957,187

; PRIOR FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/127,352

; PRIOR FILING DATE: 1999-04-01

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; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 28
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-28

```

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Query Match          98.5%; Score 5368; DB 12; Length 1018;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1013; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      17 GAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI 76
      |:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 GSGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI 61

Qy      77 YTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNFIKVLLKKND DALFVCG 136
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 YTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNFIKVLLKKND DALFVCG 121

Qy     137 TNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV 196
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 TNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV 181

Qy     197 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ 256
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ 241

Qy     257 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 316
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 301

Qy     317 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE 376
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE 361

Qy     377 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYLTKIAVDTAAGPYQNHT 436
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYLTKIAVDTAAGPYQNHT 421

Qy     437 VVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS 496
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     422 VVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS 481

Qy     497 SSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD 556
      |||||||||||||||||||||||||||||||||||||||||||||||||||

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Db	482	SSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIK EG GACSHLSPNSRLTFEQD	541
Qy	557	I ERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDST	616
Db	542	I ERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDST	601
Qy	617	DPLGAVSSHNHQDKKGVIRESYLK GHDQLVPV TLLAIAVILAFVMGAVFSGITVYCVCDH	676
Db	602	DPLGAVSSHNHQDKKGVIRESYLK GHDQLVPV TLLAIAVILAFVMGAVFSGITVYCVCDH	661
Qy	677	RRKDVAVVQRKEKELTHSRRGSMSSVTKL SGLFGDTQSKDPKPEAILTPLMHNGKLATPG	736
Db	662	RRKDVAVVQRKEKELTHSRRGSMSSVTKL SGLFGDTQSKDPKPEAILTPLMHNGKLATPG	721
Qy	737	NTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGS	796
Db	722	NTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGS	781
Qy	797	PVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK	856
Db	782	PVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK	841
Qy	857	EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDY	916
Db	842	EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDY	901
Qy	917	KRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPP PAPQRVDSIQVHSSQP	976
Db	902	KRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPP PAPQRVDSIQVHSSQP	961
Qy	977	SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP DVPPKPSFAPLSTSMKPNDACT	1030
Db	962	SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP DVPPKPSFAPLSTSMKPNDACT	1015

RESULT 8

US-10-449-548-28

; Sequence 28, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRochelle, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

```

; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 28
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-28

```

```

Query Match          98.5%; Score 5368; DB 15; Length 1018;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1013; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      17 GAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMNGTLYIAARDHI 76
      |:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 GSGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMNGTLYIAARDHI 61

Qy      77 YTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKND DALFVCG 136
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 YTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKND DALFVCG 121

Qy     137 TNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV 196
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 TNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV 181

Qy     197 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ 256
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ 241

Qy     257 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 316
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 301

Qy     317 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPPERVPKPRPGCCAGSSSLE 376
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPPERVPKPRPGCCAGSSSLE 361

Qy     377 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT 436
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT 421

```

Qy	437	VVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMLDRAS	496
Db	422	VVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMLDRAS	481
Qy	497	SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD	556
Db	482	SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD	541
Qy	557	IERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLDSPDST	616
Db	542	IERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLDSPDST	601
Qy	617	DPLGAVSSSHNHQDKKGVIRESYLKGHDQLVPVTLIAIVILAFVMGAVFSGITVYCVCDH	676
Db	602	DPLGAVSSSHNHQDKKGVIRESYLKGHDQLVPVTLIAIVILAFVMGAVFSGITVYCVCDH	661
Qy	677	RRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPEAILTPLMHNGKLATPG	736
Db	662	RRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPEAILTPLMHNGKLATPG	721
Qy	737	NTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGS	796
Db	722	NTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGS	781
Qy	797	PVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK	856
Db	782	PVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK	841
Qy	857	EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDY	916
Db	842	EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDY	901
Qy	917	KRSYPTNSLTRSHQATTLKRNTN TSSNSSHL SRNQSFGRGDNPPPAPQRVDSIQVHSSQP	976
Db	902	KRSYPTNSLTRSHQATTLKRNTN TSSNSSHL SRNQSFGRGDNPPPAPQRVDSIQVHSSQP	961
Qy	977	SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT	1030
Db	962	SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT	1015

RESULT 9

US-10-403-676-18

; Sequence 18, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

```

; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 18
;   LENGTH: 1035
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-403-676-18

```

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Query Match          98.2%;   Score 5349.5;   DB 12;   Length 1035;
Best Local Similarity 98.3%;   Pred. No. 0;
Matches 1013;   Conservative    1;   Mismatches    0;   Indels    17;   Gaps    1;

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Qy	17	GAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	76
		:	
Db	2	GSGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	61
Qy	77	YTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKND DALFVCG	136
Db	62	YTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKND DALFVCG	121
Qy	137	TNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTD FLAIDAV	196
Db	122	TNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTD FLAIDAV	181
Qy	197	IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ	256
Db	182	IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ	241
Qy	257	VCKNDMGGSQRVLEKQWTSFLKARLNC SVPGDSHFYFNILQAVTDVIRINGRDVVLATFS	316
Db	242	VCKNDMGGSQRVLEKQWTSFLKARLNC SVPGDSHFYFNILQAVTDVIRINGRDVVLATFS	301
Qy	317	TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE	376
Db	302	TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE	361
Qy	377	RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT	436
Db	362	RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT	421
Qy	437	VVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	496
Db	422	VVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	481
Qy	497	SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD	556
Db	482	SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD	541
Qy	557	IERGNTDGLGDCHNSFVALN-----GHSSSLLPSTTTSDSTAQEGYES	599
Db	542	IERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSLLPSTTTSDSTAQEGYES	601
Qy	600	RGGMLDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGHDLVPVTL LAIAVILAF	659
Db	602	RGGMLDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGHDLVPVTL LAIAVILAF	661
Qy	660	VMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKP	719
Db	662	VMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKP	721
Qy	720	EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWER	779
Db	722	EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWER	781
Qy	780	NQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVA	839
Db	782	NQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVA	841
Qy	840	QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG	899

Db	842	QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG	901
Qy	900	LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGDNF	959
Db	902	LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGDNF	961
Qy	960	PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL	1019
Db	962	PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL	1021
Qy	1020	STSMKPNDACT	1030
Db	1022	STSMKPNDACT	1032

RESULT 10

US-10-449-548-18

; Sequence 18, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRochelle, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 60/234,082

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: 60/233,798

; PRIOR FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: 60/174,485

; PRIOR FILING DATE: 2000-01-04

; PRIOR APPLICATION NUMBER: 10/403,676

; PRIOR FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/384,798

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: 60/402,407

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 60/443,062

; PRIOR FILING DATE: 2003-01-28

; NUMBER OF SEQ ID NOS: 58

Db	662	VMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKP	721
Qy	720	EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWER	779
Db	722	EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWER	781
Qy	780	NQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVA	839
Db	782	NQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVA	841
Qy	840	QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG	899
Db	842	QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG	901
Qy	900	LSKRLEMHSSSYGVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLNRNQSFGRGDNP	959
Db	902	LSKRLEMHSSSYGVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLNRNQSFGRGDNP	961
Qy	960	PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL	1019
Db	962	PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL	1021
Qy	1020	STSMKPNDACT	1030
Db	1022	STSMKPNDACT	1032

RESULT 11

US-10-403-676-20

; Sequence 20, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.


```
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-20
```

```
Query Match          94.2%; Score 5134.5; DB 12; Length 998;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 975; Conservative 0; Mismatches 0; Indels 17; Gaps 1;
```

```
Qy      56 LDIQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKD 115
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 LDIQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKD 63

Qy     116 ECHNFIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVA 175
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 ECHNFIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVA 123

Qy     176 LFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFF 235
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 LFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFF 183

Qy     236 FREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSPVGDSSHFYFNI 295
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 FREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSPVGDSSHFYFNI 243
```

Qy	296	LQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTP	355
Db	244	LQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTP	303
Qy	356	VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM	415
Db	304	VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM	363
Qy	416	VRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSE	475
Db	364	VRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSE	423
Qy	476	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGW	535
Db	424	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGW	483
Qy	536	IKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCCHNSFVALN-----GH	578
Db	484	IKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCCHNSFVALNDISTPLPDNEMSYNTVYGH	543
Qy	579	SSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESY	638
Db	544	SSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESY	603
Qy	639	LKGHDQLVPVTL LLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSR RGS	698
Db	604	LKGHDQLVPVTL LLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSR RGS	663
Qy	699	MSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQH HLDLTALPTP	758
Db	664	MSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQH HLDLTALPTP	723
Qy	759	ESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGSPVIPTDLPLRASPSHIP SVVVL	818
Db	724	ESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGSPVIPTDLPLRASPSHIP SVVVL	783
Qy	819	PITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL P	878
Db	784	PITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL P	843
Qy	879	PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATT LKRN	938
Db	844	PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATT LKRN	903
Qy	939	TNSSNSSHL SRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS	998
Db	904	TNSSNSSHL SRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS	963
Qy	999	GLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT	1030
Db	964	GLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT	995

RESULT 12

US-10-449-548-20

; Sequence 20, Application US/10449548

```

; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-20

```

```

Query Match          94.2%; Score 5134.5; DB 15; Length 998;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 975; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

```

```

Qy      56 LDIQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKD 115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4  LDIQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKD 63

Qy     116 ECHNFIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVA 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64  ECHNFIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVA 123

```

Qy	176	LFADGKLYSATVTDFLAIDAVIYRSLGESPTLRVTKHDSKWLKEPYFVQAVDYGDIYFF	235
Db	124	LFADGKLYSATVTDFLAIDAVIYRSLGESPTLRVTKHDSKWLKEPYFVQAVDYGDIYFF	183
Qy	236	FREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNI	295
Db	184	FREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNI	243
Qy	296	LQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTP	355
Db	244	LQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTP	303
Qy	356	VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM	415
Db	304	VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM	363
Qy	416	VRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSE	475
Db	364	VRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSE	423
Qy	476	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGW	535
Db	424	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGW	483
Qy	536	IKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GH	578
Db	484	IKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSINTVYGH	543
Qy	579	SSSLLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNDKKGVIRESY	638
Db	544	SSSLLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNDKKGVIRESY	603
Qy	639	LKGHDQLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGS	698
Db	604	LKGHDQLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGS	663
Qy	699	MSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTP	758
Db	664	MSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTP	723
Qy	759	ESTPTLQQKRKPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVL	818
Db	724	ESTPTLQQKRKPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVL	783
Qy	819	PITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLP	878
Db	784	PITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLP	843
Qy	879	PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNN	938
Db	844	PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNN	903
Qy	939	TNSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS	998
Db	904	TNSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS	963
Qy	999	GLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT	1030

RESULT 13

US-10-403-676-30

; Sequence 30, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: LaRochelle, William J.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Li, Li

; APPLICANT: Liu, Xiaohong

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Millet, Isabelle

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Patturajan, Meera

; APPLICANT: Peyman, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Reiger, Daniel

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE

; FILE REFERENCE: 21402-573B

; CURRENT APPLICATION NUMBER: US/10/403,676

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 09/957,187

; PRIOR FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/127,352

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 09/538,092

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: 09/604,286

; PRIOR FILING DATE: 2000-06-22

```

; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 30
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-30

```

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Query Match          93.8%; Score 5113.5; DB 12; Length 981;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 1; Indels 55; Gaps 1;

```

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 60
        |
Db      4 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 63
        |

Qy     61 IMIMNGTLYIAARDHIYTV DIDTSHTEEEIYCSKKLTWKS RQADV DTCRMKGKHKDECHNF 120
        |
Db     64 IMIMNGTLYIAARDHIYTV DIDTSHTEEEIYCSKKLTWKS RQADV DTCRMKGKHKDECHNF 123
        |

Qy    121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPF GDEFSGMARC PYDAKHANVALFADG 180
        |
Db    124 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPF GDEFSGMARC PYDAKHANVALFADG 183
        |

Qy    181 KLYSATVTDF LAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240
        |
Db    184 KLYSATVTDF LAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 243
        |

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVT 300
        |
Db    244 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVT 303
        |

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
        |
Db    304 DVIRIKGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 363
        |

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR YRL 420
        |
Db    364 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR YRL 423
        |

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 480
        |
Db    424 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 483
        |

Qy    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHKGCKKTCIASRDPYCGWIKEGG 540
        |
Db    484 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHKGCKKTCIASRDPYCGWIKEGG 543
        |

Qy    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600
        |

```

Db	544	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	579
Qy	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQQDKKGVIRESYLKGHDLVPVTLIAIVILAFV	660
Db	580	-----GVIRESYLKGHDLVPVTLIAIVILAFV	608
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	609	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE	668
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	669	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	728
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	840
Db	729	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	788
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	789	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	848
Qy	901	SKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLNRNQSFGRGDNPP	960
Db	849	SKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLNRNQSFGRGDNPP	908
Qy	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	1020
Db	909	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	968
Qy	1021	TSMKPNDACT	1030
Db	969	TSMKPNDACT	978

RESULT 14

US-10-449-548-30

; Sequence 30, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRochelle, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

```

; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 30
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-30

```

```

Query Match          93.8%; Score 5113.5; DB 15; Length 981;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 1; Indels 55; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
        |||
Db      4 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 63

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120
        |||
Db     64 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 123

Qy    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADG 180
        |||
Db    124 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADG 183

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
        |||
Db    184 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 243

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
        |||
Db    244 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 303

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
        |||
Db    304 DVIRIKGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 363

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
        |||
Db    364 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 423

```


Qy 421 TKIAVDTAAGPYQNHTVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYD 480
 |||||
 Db 424 TKIAVDTAAGPYQNHTVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYD 483

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWKEGG 540
 |||||
 Db 484 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWKEGG 543

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600
 |||||
 Db 544 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN----- 579

Qy 601 GGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLKGHDQLVPVTL LAI AVILA FV 660
 |||||
 Db 580 -----GVIRESYLKGHDQLVPVTL LAI AVILA FV 608

Qy 661 MGA VFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKL SGLFGDTQSKDPKPE 720
 |||||
 Db 609 MGA VFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKL SGLFGDTQSKDPKPE 668

Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN 780
 |||||
 Db 669 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN 728

Qy 781 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ 840
 |||||
 Db 729 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ 788

Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
 |||||
 Db 789 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 848

Qy 901 SKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPP 960
 |||||
 Db 849 SKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPP 908

Qy 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS 1020
 |||||
 Db 909 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS 968

Qy 1021 TSMKPNDACT 1030
 |||||
 Db 969 TSMKPNDACT 978

RESULT 15

US-10-403-676-46

; Sequence 46, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 46
; LENGTH: 971
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-46

Query Match 93.8%; Score 5109.5; DB 12; Length 971;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 970; Conservative 1; Mismatches 0; Indels 59; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
      |||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120
      |||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120

Qy    121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
      |||
Db    121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRV KHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
      |||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLRV KHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
      |||
Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKRWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPV PDER 360
      |||
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPV PDER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
      |||
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR--- 417

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 480
      |||
Db    418 -----CSYD 421

Qy    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG 540
      |||
Db    422 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG 481

Qy    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600
      |||
Db    482 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 541

Qy    601 GGMLDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGHDQLVPV TLLAIAVILAFV 660
      |||
Db    542 GGMLDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGHDQLVPV TLLAIAVILAFV 601

Qy    661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE 720
      |||
Db    602 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE 661

Qy    721 AILTPLMHNGK LATPGNTAKMLIKADQHHL DLTALPTPESTPTLQQKRKPSRGSR EWERN 780
      |||
Db    662 AILTPLMHNGK LATPGNTAKMLIKADQHHL DLTALPTPESTPTLQQKRKPSRGSR EWERN 721

Qy    781 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVL PITQQGYQHEYVDQPKMSEVAQ 840
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Db	722	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	781
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	782	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	841
Qy	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTILKRNTNSSNSSHLNRNQSFGRGDNPP	960
Db	842	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTILKRNTNSSNSSHLNRNQSFGRGDNPP	901
Qy	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	1020
Db	902	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	961
Qy	1021	TSMKPNDACT	1030
Db	962	TSMKPNDACT	971

Search completed: March 24, 2004, 13:19:31
Job time : 77.7731 secs

OM protein - protein search, using sw model

Run on: March 24, 2004, 13:11:03 ; Search time 71.9691 Seconds
(without alignments)
4515.598 Million cell updates/sec

Title: US-09-856-681A-2
Perfect score: 5450
Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description

1	5024.5	92.2	1005	11	Q9EQ71	Q9eq71 mus musculu
2	3677	67.5	699	4	Q96SW4	Q96sw4 homo sapien
3	2980.5	54.7	574	4	Q96SM8	Q96sm8 homo sapien
4	2963	54.4	587	11	Q8BUT0	Q8but0 mus musculu
5	2961	54.3	605	11	Q8BXZ7	Q8bxz7 mus musculu
6	2952	54.2	562	4	Q96SY4	Q96sy4 homo sapien
7	2947	54.1	562	4	Q8NC49	Q8nc49 homo sapien
8	2621.5	48.1	507	4	Q96T04	Q96t04 homo sapien
9	2368	43.4	1073	4	Q8Nfy4	Q8nfy4 homo sapien
10	2349	43.1	1017	4	Q8Nfy5	Q8nfy5 homo sapien
11	2315.5	42.5	998	4	Q8Nfy6	Q8nfy6 homo sapien
12	2314	42.5	1011	4	Q8Nfy3	Q8nfy3 homo sapien
13	2314	42.5	1022	4	Q9P249	Q9p249 homo sapien
14	2309.5	42.4	1009	11	Q80TD0	Q80td0 mus musculu
15	2213	40.6	418	4	Q96JU9	Q96ju9 homo sapien
16	1908.5	35.0	595	11	Q8BKG8	Q8bkg8 mus musculu
17	1876.5	34.4	687	4	Q9BXR8	Q9bxr8 homo sapien
18	1611	29.6	476	4	Q8Nfy7	Q8nfy7 homo sapien
19	1526.5	28.0	963	11	Q91Y36	Q91y36 mus musculu
20	1480.5	27.2	452	13	Q7T165	Q7t165 brachydanio
21	1386.5	25.4	367	4	Q9HAH9	Q9hah9 homo sapien
22	1355.5	24.9	923	11	Q8R4U3	Q8r4u3 mus musculu
23	1320	24.2	920	11	Q8R4U4	Q8r4u4 rattus norv
24	1059	19.4	366	13	Q7ZV83	Q7zv83 brachydanio
25	856.5	15.7	770	5	O44253	O44253 drosophila
26	854.5	15.7	770	5	Q9V3M4	Q9v3m4 drosophila
27	847.5	15.6	774	13	Q8JIW9	Q8jiw9 xenopus lae
28	823.5	15.1	844	11	Q8BXU8	Q8bxu8 mus musculu
29	817.5	15.0	748	4	Q8TB71	Q8tb71 homo sapien
30	802.5	14.7	777	11	Q8BMF6	Q8bmf6 mus musculu
31	802.5	14.7	777	11	Q8BH34	Q8bh34 mus musculu
32	779.5	14.3	724	5	Q9V7Q7	Q9v7q7 drosophila
33	771	14.1	1122	11	Q7TT33	Q7tt33 mus musculu
34	768	14.1	697	5	Q8MLF1	Q8mlf1 drosophila
35	763	14.0	635	4	Q96GX0	Q96gx0 homo sapien
36	749	13.7	756	13	Q8QGU9	Q8qgu9 gallus gall
37	748	13.7	775	11	Q9QX23	Q9qx23 mus musculu
38	736.5	13.5	799	11	Q8BJC1	Q8bjc1 mus musculu
39	735.5	13.5	862	4	Q7Z5S4	Q7z5s4 homo sapien
40	694.5	12.7	616	5	Q9V7P8	Q9v7p8 drosophila
41	693	12.7	963	4	Q9C0C4	Q9c0c4 homo sapien
42	686	12.6	782	4	Q9NS98	Q9ns98 homo sapien
43	666.5	12.2	1083	5	Q9VTT0	Q9vtt0 drosophila
44	666.5	12.2	1091	5	Q7YU67	Q7yu67 drosophila
45	660	12.1	823	11	Q8BIR6	Q8bir6 mus musculu

ALIGNMENTS

RESULT 1

Q9EQ71

ID	Q9EQ71	PRELIMINARY;	PRT; 1005 AA.
AC	Q9EQ71;		
DT	01-MAR-2001	(TrEMBLrel. 16, Created)	
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	

DE Axon guidance signal SEMA6A1.
 GN SEMA6A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20564339; PubMed=10993894;
 RA Klostermann A., Lutz B., Gertler F., Behl C.;
 RT "The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-
 RT 1/Sema6A-1) bind to the Enabled/Vasodilator-stimulated Phosphoprotein-
 RT like Protein (EVL) via a novel carboxyl-terminal Zyxin-like domain.";
 RL J. Biol. Chem. 275:39647-39653(2000).
 DR EMBL; AF288666; AAG29494.1; -.
 DR MGD; MGI:1203727; Sema6a.
 DR GO; GO:0016021; C:integral to membrane; ISS.
 DR GO; GO:0008580; F:cytoskeletal regulator activity; ISS.
 DR GO; GO:0007411; P:axon guidance; ISS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; ISS.
 DR GO; GO:0007399; P:neurogenesis; ISS.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 1005 AA; 111758 MW; 57B69927F45B079D CRC64;

Query Match 92.2%; Score 5024.5; DB 11; Length 1005;
 Best Local Similarity 91.9%; Pred. No. 0;
 Matches 948; Conservative 26; Mismatches 30; Indels 27; Gaps 2;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFGVGHKPGRNTTQRHRLDIQM	60
Db	1	MRPAALLLCLTLLHCAGAGFPEDSEPISISHGNYTKQYPVFGVGHKPGRNTTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
		:	
Db	61	IMIMNRTLYVAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADG	180
		: :	
Db	121	IKVLLKKND DTLFVCGTNAFNPSCRNYRVDLTLETFGDEFSGMARCPYDAKHVNIALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
		:	
Db	181	KLYSATVTDFLAIDAVIYRSPGDSPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPPER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIADVFTGRFKEQKSPDSTWTPVPPER	360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
 |||||:|||||
 Db 361 VPKPRPGCCAGSSSLEKYATSNEFPDDTLNFIKTHPLMDEAVPSIINRPWFLRTMVRYRL 420

Qy 421 TKIAVDTAAGPYQNHTVVLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
 ||||| ||||| |||||:||| |||||
 Db 421 TKIAVDNAAGPYQNHTVV-----FLEEMNVYNPEKCSYD 454

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540
 ||||| ||||| |||||:| |
 Db 455 GVEDKRIMGMQLDRASGSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWVRESG 514

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600
 :|:|||| |||||:||| |:||||| ::|||
 Db 515 SCAHLSPLSRLTFEQDIERGNTDGLGDCHNSFVALNGHASSLYPNTTTSDSASRDGYESR 574

Qy 601 GGMLDWKHLLDSPDSTDPLGAVSSHNHQQDKKGVIRESYLKGHDLVLPVTLIAIVILAFV 660
 ||||| ||:| |||||:|||||
 Db 575 GGMLDWNLDLEAPGSTDPLGAVSSHNHQQDKKGVIRESYLKSNDQLVLPVTLIAIVILAFV 634

Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE 720
 ||||| |||||:|||||:|
 Db 635 MGAVFSGIIVYCVCDHRRKDVAVVRRKEKELTHSRGSMSSVSELSGLFGDTQSKDPKPE 694

Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSRREWERN 780
 ||||| |||||:|||||
 Db 695 AILTPLMHNGKLATSSNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPNRGSRREWERN 754

Qy 781 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSE-VA 839
 ||:||||| ||
 Db 755 QNIINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVVA 814

Qy 840 QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG 899
 ||||| ||||| |||||
 Db 815 QMALEDQAATLEYKTTKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGTSLSQTG 874

Qy 900 LSKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQATTLLKRNTNSSNSSHLNRNQSFGRGDNP 959
 ||||| |||||:| ||||| |||||
 Db 875 LSKRLEMQHSSSYGLEKRSYPTNSLTRSHQTTTLKRNTNSSNSSHLNRNQSFGRGDNP 934

Qy 960 PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL 1019
 ||||| ||||| ||||| |||||
 Db 935 PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL 994

Qy 1020 STSMKPNDACT 1030
 |||||
 Db 995 STSMKPNDACT 1005

RESULT 2

Q96SW4

ID Q96SW4 PRELIMINARY; PRT; 699 AA.

AC Q96SW4;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein FLJ14595.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK027501; BAB55158.1; -.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 699 AA; 76723 MW; 2E5F111D59741394 CRC64;

Query Match 67.5%; Score 3677; DB 4; Length 699;
 Best Local Similarity 100.0%; Pred. No. 4.5e-291;
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	332	MLDIASVFTGRFKEQKSPDSTWTPVDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF	391
Db	1	MLDIASVFTGRFKEQKSPDSTWTPVDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF	60
Qy	392	IKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFL	451
Db	61	IKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFL	120
Qy	452	ARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP	511
Db	121	ARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP	180
Qy	512	LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS	571
Db	181	LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS	240
Qy	572	FVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNDKDK	631
Db	241	FVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNDKDK	300
Qy	632	GVIRESYLK GHDQLVPVTL LAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKEL	691
Db	301	GVIRESYLK GHDQLVPVTL LAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKEL	360
Qy	692	THSR RGSMS SVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHL	751
Db	361	THSR RGSMS SVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHL	420
Qy	752	LTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSH	811

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Db      421  |LTALPTPESTPTLQQKQKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSH| 480
Qy      812  |IPSVVVLPIITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV| 871
Db      481  |IPSVVVLPIITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV| 540
Qy      872  |ENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA| 931
Db      541  |ENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA| 600
Qy      932  |TTLKRNTNTSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNA| 991
Db      601  |TTLKRNTNTSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNA| 660
Qy      992  |YNSLTRSGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT| 1030
Db      661  |YNSLTRSGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT| 699

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RESULT 3

Q96SM8

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ID   Q96SM8          PRELIMINARY;          PRT;          574 AA.
AC   Q96SM8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein FLJ14748.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK027654; BAB55269.1; -.
DR   GO; GO:0007275; P:development; IEA.
DR   InterPro; IPR003659; Plexin-like.
DR   SMART; SM00423; PSI; 1.
KW   Hypothetical protein.
SQ   SEQUENCE 574 AA; 62822 MW; 0C79E01A4117A495 CRC64;

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Query Match          54.7%;  Score 2980.5;  DB 4;  Length 574;
Best Local Similarity 90.7%;  Pred. No. 2.5e-234;
Matches 574;  Conservative 0;  Mismatches 0;  Indels 59;  Gaps 1;

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Qy      398  |MDEAVPSIFNRPWFLRTMVRYLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNS| 457
Db      1    |MDEAVPSIFNRPWFLRTMVR-----| 20

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Qy	458	GFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCER	517
Db	21	-----CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCER	61
Qy	518	HGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG	577
Db	62	HGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG	121
Qy	578	HSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRE	637
Db	122	HSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRE	181
Qy	638	YLKGHQQLVPVTLIAIVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRG	697
Db	182	YLKGHQQLVPVTLIAIVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRG	241
Qy	698	SMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPT	757
Db	242	SMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPT	301
Qy	758	PESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVV	817
Db	302	PESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVV	361
Qy	818	LPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL	877
Db	362	LPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL	421
Qy	878	PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRN	937
Db	422	PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRN	481
Qy	938	NTNSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR	997
Db	482	NTNSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR	541
Qy	998	SGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT	1030
Db	542	SGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT	574

RESULT 4

Q8BUT0

ID Q8BUT0 PRELIMINARY; PRT; 587 AA.
AC Q8BUT0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sema domain.
GN A730020P05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK082711; BAC38582.1; -.
 DR MGD; MGI:2443196; A730020P05Rik.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 587 AA; 66044 MW; EB9C7B102C4DB97A CRC64;

Query Match 54.4%; Score 2963; DB 11; Length 587;
 Best Local Similarity 95.1%; Pred. No. 7e-233;
 Matches 549; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Db	1	MRPAALLLCLTLLHCAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF	120
		:	
Db	61	IMIMNRTLYVAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
		: :	
Db	121	IKVLLKKND DTLFVCGTNAFNPSCRNYRVDLTLETFGDEFSGMARCPYDAKHANIALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
		:	
Db	181	KLYSATVTDFLAIDAVIYRSLGDSPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
		:	
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIANVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
		:	
Db	361	VPKPRPGCCAGSSSLEKYATSNEFPDDTLNFIKTHPLMDEAVPSIINRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYD	480
		: :	
Db	421	TKIAVDNAAGPYQNHTVVFLGSEKGIILKFLARIGSSGFLNGSLFLEEMNVYNPEKCSYD	480
Qy	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWIKEGG	540
		:	
Db	481	GVEDKRIMGMLDRASGSLYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWVRESG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG	577
		: :	
Db	541	SCAHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG	577

Q8BXZ7

Query Match 54.3%; Score 2961; DB 11; Length 605;
Best Local Similarity 94.5%; Pred. No. 1.1e-232;
Matches 550; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Db	1	MRPAALLLCLTLLHCAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
Db	61	IMIMNRTLYVAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Db	121	IKVLLKKND DTLFVCGTNAFNPS CRNYRVDTLETFGDEFSGMARCPYDAKHANIALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFFREIA	240
Db	181	KLYSATVTDFLAIDAVIYRSLGDSPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFFREIA	240
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360

Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIANVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
		:	
Db	361	VPKPRPGCCAGSSSLEKYATSNEFPDDTLNFIKTHPLMDEAVPSIINRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYD	480
		: :	
Db	421	TKIAVDNAAGPYQNHTVVFLGSEKGIILKFLARIGSSGFLNGSLFLEEMNVYNPEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHKGCKKTCIASRDPYCGWIKEGG	540
		:	
Db	481	GVEDKRIMGMQLDRASGSLYVAFSTCVIKVPLGRGERHKGCKKTCIASRDPYCGWVRESG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSL	582
		: :	
Db	541	SCHLSPLSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPL	582

RESULT 6

ID Q96SY4 PRELIMINARY; PRT; 562 AA.

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein FLJ14565.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Ninomiya K., Iwayanagi T.;

RT "NEDO human cDNA sequencing project.";

RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AK027471; BAB55136.1; -.

DR GO; GO:0007275; P:development; IEA.

DR InterPro; IPR003659; Plexin-like.

DR SMART; SM00423; PSI; 1.

KW Hypothetical protein.

SEQUENCE 562 AA; 61313 MW; 6AB3685FAD1DD78A CRC64;

Query Match 54.2%; Score 2952; DB 4; Length 562;

Best Local Similarity 100.0%; Pred. No. 5.2e-232;

Matches 562; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qv 469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIAS 528

11

Db 1 MSVYNSEKCSYDGVEDKRIMGOLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIAS 60

Qy	529	RDPCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTT	588
Db	61	RDPCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTT	120
Qy	589	SDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPV	648
Db	121	SDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPV	180
Qy	649	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGL	708
Db	181	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGL	240
Qy	709	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQR	768
Db	241	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQR	300
Qy	769	KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE	828
Db	301	KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE	360
Qy	829	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL	888
Db	361	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL	420
Qy	889	GPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTCLKRNNTNSSNSSHLS	948
Db	421	GPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTCLKRNNTNSSNSSHLS	480
Qy	949	RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP	1008
Db	481	RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP	540
Qy	1009	DVPPKPSFAPLSTSMKPNDACT	1030
Db	541	DVPPKPSFAPLSTSMKPNDACT	562

RESULT 7

Q8NC49

ID Q8NC49 PRELIMINARY; PRT; 562 AA.

AC Q8NC49;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein FLJ90494.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,

RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

RT "NEDO human cDNA sequencing project.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK074975; BAC11326.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 562 AA; 61286 MW; 708041459E34D78A CRC64;

Query Match 54.1%; Score 2947; DB 4; Length 562;
 Best Local Similarity 99.8%; Pred. No. 1.3e-231;
 Matches 561; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	469	MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIAS	528
Db	1	MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIAS	60
Qy	529	RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT	588
Db	61	RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT	120
Qy	589	SDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPV	648
Db	121	SDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPV	180
Qy	649	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGL	708
Db	181	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGL	240
Qy	709	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKR	768
Db	241	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKR	300
Qy	769	KPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHE	828
Db	301	KPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHE	360
Qy	829	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL	888
Db	361	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL	420
Qy	889	GPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTN SSNSSHLS	948
Db	421	GPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTN SSNSSHLS	480
Qy	949	RNQSFGRGDNPPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP	1008
Db	481	RNQSFGRGDSPPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP	540
Qy	1009	DVPPKPSFAPLSTSMKPNDACT	1030
Db	541	DVPPKPSFAPLSTSMKPNDACT	562

RESULT 8

Q96T04

ID Q96T04 PRELIMINARY; PRT; 507 AA.

AC Q96T04;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein FLJ14533.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK027439; BAB55111.1; -.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003659; Plexin-like.
 DR SMART; SM00423; PSI; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 507 AA; 55464 MW; 8CC567B438C51B39 CRC64;

Query Match 48.1%; Score 2621.5; DB 4; Length 507;
 Best Local Similarity 90.2%; Pred. No. 4.3e-205;
 Matches 507; Conservative 0; Mismatches 0; Indels 55; Gaps 1;

Qy	469	MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIAS	528
Db	1	MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIAS	60
Qy	529	RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT	588
Db	61	RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	108
Qy	589	SDSTAQEGYESRGGMLDWKHLDDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDQLVPV	648
Db	109	-----GVIRESYLKGHDQLVPV	125
Qy	649	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGL	708
Db	126	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGL	185
Qy	709	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKR	768
Db	186	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKR	245
Qy	769	KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPTITQQGYQHE	828
Db	246	KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPTITQQGYQHE	305
Qy	829	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL	888
Db	306	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL	365
Qy	889	GPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRNNNTSSNSSHLS	948

Db 366 GPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTCLKRNNTNSSNSSHLS 425

Qy 949 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 1008
 |||

Db 426 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 485

Qy 1009 DVPPKPSFAPLSTSMKPNDACT 1030
 |||

Db 486 DVPPKPSFAPLSTSMKPNDACT 507

RESULT 9

Q8NFY4

ID Q8NFY4 PRELIMINARY; PRT; 1073 AA.
 AC Q8NFY4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Semaphorin 6D isoform 4.
 GN SEMA6D.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Qu X., Zhai Y., Wei H., Yu Y., Tang F., He F.;
 RT "Homo sapiens semaphorin 6D isoform 4 (SEMA6D.4) mRNA, complete cds."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF389429; AAM69452.1; -.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 1073 AA; 119872 MW; 7DCE4DFC5BF70F9E CRC64;

Query Match 43.4%; Score 2368; DB 4; Length 1073;
 Best Local Similarity 46.0%; Pred. No. 7.5e-184;
 Matches 512; Conservative 159; Mismatches 308; Indels 134; Gaps 30;

Qy 1 MRSEALLLYFTLL---HFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLD 57
 || | | || ||| ||:: :||:|||| | :| | :| |||

Db 1 MRVFLLCAYILLMLVSQLRAVSPEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD 58

Qy 58 IQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDEC 117
 |::: : |||| || :||::: | : :|||:| | : | |||

Db 59 FQLMLKIRDITLYIAGRDQVYTVNLNEMPKEVIPNKKLTWRSRQQDRENCAMKGKHKDEC 118

Qy 118 HNFIVKLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF 177
 ||||| : :||: :||| |||| || |:: || | :| ||:||||:|: | |||

Db 119 HNFIVKVFVPRNDEMVFVCGTNAFNPSCRNYRSLTLEYDGEEISGLARCPFDARQTNVALF 178

Qy 178 ADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFR 237
 ||| |||| |||||:|: |||:|:|:|:|:|: |::|:|:|:|

Db 179 ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYFFFR 238

Qy 238 EIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPGDSHFYFNILQ 297

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      |||||:| :|| |: |||:||||||| ||||| |||||:|
Db      239 EIAVEHNNLGKAVYSRVARICKNDMGGSQVRLEKHWT$FLKARLNCSVPGDSFFYFDVLQ 298

Qy      298 AVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
      :|||:|:| | : | :| |||||:| | | |||||:| | | |
Db      299 SITDIIQINGIPTVVGVTQLNSIPGSAVCAFSMDIEKVFKEQKTPDSVWTAVP 358

Qy      358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
      :||:||||||| | | | :||:|:|:|:| | | | : | | |
Db      359 EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETL$FIKSHPLMDSAVPPIADEPWFTKTRVR 418

Qy      418 YRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGF-LNDSL$FLEEMSVYNSEK 476
      |||| |:|| :|||||:|:|:| | :|| | | : | | | | |
Db      419 YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPF$SLNDSVLL$EEIEAYNHAK 476

Qy      477 CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR$CERHGKCKKTCIASRDPYCGWI 536
      || : |||: : ||| : |||||:|:|:| | |||:| |||:|
Db      477 CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPL$RCERYG$CKKSCIASRDPYCGWL 536

Qy      537 KEGGACSHLSPNSRLT-FEQDIERGNTDGLGDCHNSF$VALNGHSSSLPSTTTSDSTAQE 595
      : |:|| :|| :|| | || | |||| :||:| | |
Db      537 SQ-GSCGRVTPGMLAEGYEQDTEFGNTAHLGDCH-----EIL$PTSTTPD----- 579

Qy      596 GYESRGG-----MLD-WKHL-----DSP---D$TDP 618
      | : || :|| | : | | | | | |
Db      580 -YKIFGGPTSDMEVSSSVTTMASIPEITPKVIDTWR$PKLTSSRK$FVVQDDPNTSDFTDP 638

Qy      619 LGAVSSHHQDKKGVIRESYLKGH$DQLVPVTL$AI$VILAFV$MGAVFSGITVYCVCD-HR 677
      | : || | :|| : : | | |||:| :|: || |
Db      639 LSGI-----PKGVRWEVQSGESNQMVH$MNLITCVFAAFVL$GAFIAGVAVYCYRDMFV 691

Qy      678 RKDVAVVQRKEKELTHSRGSMSSVT$KLSGLFG----DTQ$KDPKPEAILT$PLMHNGKLA 733
      ||: : | : | | | ||:| | : | | :|
Db      692 RKNRKI--HKDAESAQ$CTDSSGSFAKL$NGLFDS$PVKEYQQNID$PKLYSNLLTSRKELP 749

Qy      734 TPGNTAKMLIKADQHHL$DLTALPTPE$TPTLQ$QKRKPSRGSREWERNQ$NLINACTKDMPP 793
      |:| | : :| ||||| | | : | : : : | |:|
Db      750 PNGDTKSMVMDHRGQ$PPELAALPTPE$TPVLH$QKTLQAMKSHSEKAHGH--GASR$KETPQ 807

Qy      794 MGSPVIPTDLPLRAS$SHIPSVVVL$PITQ$QGYQHEY-----VDQ$P---KMS 836
      | | | | ||| :|| | : : |||:| | |
Db      808 FFPSSPPPH$PL--SHGHIPSAIVL$PNATHDYNT$SFSNSNAHKA$EKKLQ$NIDHPLTKSSS 865

Qy      837 EVAQMALEDQAATLEYKTIKEHL$SSKSPN-----HG$VNLVENL$DSL---PPKVP 882
      : | | | :||: : | | : : : | : ||||
Db      866 KR$HRRSVDSRNTL--NDLLKHLNDP$NSNP$KAIMGDIQMAH$QNLMLDPMGSMSEVPPKVP 923

Qy      883 QREASLGPPGASLSQTGL$SKRLEMHHSSSY---GVDYKRSYPT$NLSL$TRSHQATTLKRNNT 939
      |||| | :| : :||: : : : :| | | | : : : |
Db      924 NREASLYSP$STLPRNSPTK$RVDVPTTPGVPMT$SLERQ$GYHKNSSQR-HSISAMPK-NL 981

Qy      940 NSSNSSHL$SRNQSFGRGD-NPP$PAPQ$RVD$SIQVHSSQ$PSGQAVTVSRQ$PSLNAYNSLT-- 996
      || | || | | | :|| | | | :| ||||: :| |
Db      982 NSPNGVLLSRQ$PSMNRGGYMP$TPTGAKVDYIQ-----GTPV$SVHLQ$PSLSRQ$SSYTSN 1034

Qy      997 ----R$GLKRT$PSL$KPDVPPK$SFAPL$TSMKP 1025
      |:||||||| | : |:|

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      ::||| ||| | | || :||:|:|:| ||| | | : ||| :| ||
Db      359 EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSEFIKSHPLMDSAPVPIADEPWFTKTRVR 418
Qy      418 YRLTKIAVDTAAGPYQNHTVVLGSEKGIILKFLARIGNSGF-LNDSLFLLEEMSVYNSEK 476
      ||| | :|| :||| | :||:| ||| | :|| ||: | | |||: ||: | | |
Db      419 YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPFSLNDSVLLEEIEAYNHAK 476
Qy      477 CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWI 536
      || : |||::: :||: :||| | :||:| |||:| |||:| |||:| |||:|
Db      477 CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSCKKSCIASRDPYCGWL 536
Qy      537 KEGGACSHLSPNSRLT-FEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQE 595
      : | :| :| :|| | || | ||| | :||:| | |
Db      537 SQ-GSCGRVTPGMLAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD----- 579
Qy      596 GYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDQLVPVTLIAIAV 655
      | : || | | | | | | | | | | | | | | :| :| :| |
Db      580 -YKIFGG-----PTS-----GVRWEVQSGESNQMVHNMVNLITCV 612
Qy      656 ILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFG---- 710
      |||:| | :| :|| | ||: : | :| | | | | | :|||
Db      613 FAAFVLGAFIAGVAVYCYRDMFVRKNRKI--HKDAESAQSCTDSSGSFAKLNGLFDSPVK 670
Qy      711 DTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKP 770
      : | :| :| :| :| :| :| :| ||| ||| | | |
Db      671 EYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPTPESTPVLHQKTLQ 730
Qy      771 SRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEY- 829
      : | : : : | :| | | | | | | | | | | :
Db      731 AMKSHSEKAHGH--GASRKETPQFFPSSPPPHSPL--SHGHIPSAIVLPNATHDYNTSFS 786
Qy      830 -----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPN----- 865
      :| | | : | | | :||: :|
Db      787 NSNAHKAEEKLQNI DHPLTKSSSKRDHRRSVDSRNTL--NDLLKHLNDPNSNPKAIMGDI 844
Qy      866 ---HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSY---GVDY 916
      | : : : | : ||| | ||| | :| : :||: : :
Db      845 QMAHQNLMLDPMGSMSEVPKVENREASLYSPSTLPRNSPTKRVDVPTTPGVPMTSLER 904
Qy      917 KRSYPTNSLTRSHQATTLKRNNNTSSNSSHLNRNQSFGRGD-NPPAPQVRVDSIQVHSSQ 975
      :| | || | | : : : | | | ||| | || | | :| | |
Db      905 QRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRGGYMPPTPTGAKVDYIQ----- 957
Qy      976 PSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPPKPSFAPLSTSMKP 1025
      | | :| |||: :| | | :||| ||| ||| ||| | | :| :|
Db      958 --GTPVSVHLQPSLSRQSSYTSNGTLPTGLKRTPSLKPDVPPKPSFVPQTPSVRP 1011

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RESULT 11

Q8NFY6

ID Q8NFY6 PRELIMINARY; PRT; 998 AA.

AC Q8NFY6;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Semaphorin 6D isoform 2.

GN SEMA6D.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Qu X., Zhai Y., Wei H., Yu Y., Tang F., He F.;
 RT "Homo sapiens semaphorin 6D isoform 2 (SEMA6D.2) mRNA, complete cds."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF389427; AAM69450.1; -.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 998 AA; 111730 MW; 3F46D6872E8D5344 CRC64;

Query Match 42.5%; Score 2315.5; DB 4; Length 998;
 Best Local Similarity 45.8%; Pred. No. 1.3e-179;
 Matches 493; Conservative 155; Mismatches 293; Indels 135; Gaps 26;

Qy	1	MRSEALLLYFTLL---HFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLD	57
		:: : :: : :	
Db	1	MRVFLLCAYILLMLVSQLRAVSFPEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD	58
Qy	58	IQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDEC	117
		::: : : ::: : : : :	
Db	59	FQLMLKIRDITLYIAGRDQVYTVNLNEMPKEVIPNKKLTWRSRQQDRENCAMKGKHKDEC	118
Qy	118	HNFIKVLKKND DALFVCGTNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALF	177
		: : : :: : : :	
Db	119	HNFIKVFVPRNDEMVFVCGTNAFNPMCRYRLSTLEYDGEEISGLARCPFDARQTNVALF	178
Qy	178	ADGKLYSATVTDFLAIDAVIYRSLGESPTLRVTKHDSKWLKEPYFVQAVDYGDYIYFFFR	237
		: : : : : : : : : : :	
Db	179	ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYFFFR	238
Qy	238	EIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSSHFYFNILQ	297
		: : : :: :	
Db	239	EIAVEHNNLGKAVYSRVARICKNDMGGSQRVLEKHWT SFLKARLNCSVPGDSFFYFDVLQ	298
Qy	298	AVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP	357
		:: : : : : : :	
Db	299	SITDIIQINGIPTVVGVFETTQLNSIPGSAVCAFSMDIEKVKGRFKEQKTPDSVWTAVP	358
Qy	358	DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR	417
		:: : : : : : : :	
Db	359	EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSFIKSHPLMDSAVPPIADEPWFTKTRVR	418
Qy	418	YRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGF-LNDSL FLEEMSVYNSEK	476
		: : : : : ::: : : :	
Db	419	YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPFSLNDSVLLLEEIEAYNHAK	476
Qy	477	CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWI	536
		: :: : : : : : : : :	
Db	477	CSAENEEDKKVISLQLDKDHALYVAFSSCIIRIPLSRCERYGSCKKSCIASRDPYCGWL	536
Qy	537	KEGGACSHLSPNSRLT-FEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQE	595

```

      : |:| ::| :||| | ||| |||||
Db      537 SQ-GSCGRVTPGMLAEGYEQDTEFGNTAHLGDCHG----- 570

Qy      596 GYESRGGMLDWKHLSDSPDSTDPLGAVSSSHNHQDKKGVIRESYLKGHDLVPVTLTLLAIAV 655
      : |:| :| :| :|:| : :| |
Db      571 -----VRWE--VQSGES-----NQMVHNMVNLITCV 593

Qy      656 ILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFG---- 710
      |||:| :|: ||| | ||: : |:| | | ||:|
Db      594 FAAFVLGAFIAGVAVYCYRDMFVRKNRKI--HKDAESAQSCTDSSGSFAKLNGLFDSPVK 651

Qy      711 DTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKP 770
      : | |:| | :| |:| |:: :| ||||| | ||
Db      652 EYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPTPESTPVLHQKTLQ 711

Qy      771 SRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEY- 829
      : | : : : | |:| | || | ||| :|| | :
Db      712 AMKSHSEKAHGH--GASRKETPQFFPSPPPHSPL--SHGHIPSAIVLPNATHDYNTSFS 767

Qy      830 -----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPN----- 865
      :| | |:| | || :||: :|
Db      768 NSNAHKAEEKLQNIHPLTKSSSKRDHRRSVDSRNTL--NDLLKHLNDPNSNPKAIMGDI 825

Qy      866 ---HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSY---GVDY 916
      | ::: :|: |||| |||| |::| : :||:: : :
Db      826 QMAHQNLMLDPMGSMSEVPKVPNREASLYSPSTLPRNSPTKRVDVPTTPGVPMTSLER 885

Qy      917 KRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGD-NPPPAPQRVDSIQVHSSQ 975
      :| | || | | : : : | || | || | | | :|| |
Db      886 QRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRGGYMPPTGAKVDYIQ----- 938

Qy      976 PSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPPKPSFAPLSTSMKP 1025
      | |:| |||: :| | |:| ||||| ||||| | :|:|
Db      939 --GTPVSVHLQPSLSRQSSYTSNGTLPRTLGLKRTPSLKPDVPPKPSFVPQTPSVRP 992

```

RESULT 12

Q8NFY3

```

ID   Q8NFY3          PRELIMINARY;          PRT;   1011 AA.
AC   Q8NFY3;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Semaphorin 6D isoform 1.
GN   SEMA6D.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Qu X., Wei H., Zhai Y., Yu Y., Tang F., He F.;
RT   "Homo sapiens semaphorin 6D isoform 1 (SEMA6D.1) mRNA, complete cds.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF389430; AAM69453.1; -.
DR   InterPro; IPR001627; Sema.

```

DR Pfam; PF01403; Sema; 1.
DR SMART; SM00630; Sema; 1.
SQ SEQUENCE 1011 AA; 113289 MW; 9D6B8B3633941B89 CRC64;

Query Match 42.5%; Score 2314; DB 4; Length 1011;
Best Local Similarity 45.4%; Pred. No. 1.8e-179;
Matches 494; Conservative 155; Mismatches 292; Indels 148; Gaps 26;

```
Qy      1 MRSEALLLYFTLL---HFAGAGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQRHRLD 57
      || | | | | ||| ||:: :|::| | | | :| | | | |
Db      1 MRVFLLCAYILLMVSQLRVASFPEDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD 58

Qy     58 IQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDEC 117
      |::: : | | | | || :| | |::: :| :| | | | | | | :| | | | | |
Db     59 FQLMLKIRDTLTYIAGRDQVYTVNLNEMPKTEVIPNKKLTWRSRQQDRENCAMKGKHKDEC 118

Qy    118 HNFIVKLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF 177
      | | | | | : :| :| | | | | | | | | | :| | | | | :| :| | | |
Db    119 HNFIVKVFVRNDEMVFVCGTNAFNPMCRYRLSTLEYDGEEISGLARCPFDARQTNVALF 178

Qy    178 ADGKLYSATVTDFLAIDAVIYRSLGESPTLRVTKHDSKWLKEPYFVQAVDYGDIYFFFR 237
      | | | | | | | | | | | | | | | | :| :| :| :| :| :| :| :| :| :|
Db    179 ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYFFFR 238

Qy    238 EIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQ 297
      | | | | :| :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    239 EIAVEHNNLGKAVYSRVARICKNDMGGSQRVLEKHWT SFLKARLNCSVPGDSFFYFDVLQ 298

Qy    298 AVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
      :| :| :| :| | :| :| | | | | | | | | | | | | | | | | | | |
Db    299 SITDIIQINGIPTVVGVFETTQLNSIPGSAVCAFSMDDIEKVFKGRFKEQKTPDSVWTAVP 358

Qy    358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
      :| :| | | | | | | | | | | :| :| :| :| :| :| :| :| :| :| :|
Db    359 EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETL SFIKSHPLMDSAVPPIADEPWFETKTRVR 418

Qy    418 YRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGF-LNDSL FLEEMSVYNSEK 476
      | | | | :| :| :| | | | :| :| :| :| :| :| :| :| :| :| :| :|
Db    419 YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPFSLNDSV LLEEIEAYNHAK 476

Qy    477 CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWI 536
      | | : | | | :| :| :| :| :| | | | | :| :| :| :| :| :| :| :|
Db    477 CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSCCKKSCIASRDPYCGWL 536

Qy    537 KEGGACSHLSPNSRLT-----FEQDIERGNTDGLGDCHNSFVALNGHSSSL 582
      :| :| :| | | | | | | :| | | | | | | | | |
Db    537 SQ-GSCGRVTPGMLLLLTEDFFAFHNHSAEGYEQDTEFGNTAHLGDCHG----- 583

Qy    583 LPSTTTSDSTAQEGYESRGGMLDWKHL LDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGH 642
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    584 -----VRWE--VQSGES----- 593

Qy    643 DQLVPVTL LAIAVILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRRGSMSS 701
      :| :| :| :| | | | :| :| | | | | :| :| :| :| :| :| :| :|
Db    594 NQMVHMNVLITCVFAAFVLGAFIAGVAVYCYRDMFVRKNRKI--HKDAESAQSCTDSSGS 651

Qy    702 VTKLSGLFG---DTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPT 757
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      ||:||||      : |      | :      |      :|      |:|      |::      :|      ||||
Db      652 FAKLNGLFDSVPKEYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPT 711

Qy      758 PESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVV 817
      ||||| | ||      : |      : : :      | | : |      |      ||      |      |||| :|
Db      712 PESTPVLHQKTLQAMKSHSEKAHGH--GASRKETPQFFPSSPPPHSPL--SHGHIPIAIV 767

Qy      818 LPITQQGYQHEY-----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLS 860
      ||      |      :      :| |      | :      |      ||      : :||:
Db      768 LPNATHDYNTSFSNSNAHKAEEKKLQNIHPLTKSSSKRDHRSVDSRNTL--NDLLKHLN 825

Qy      861 SKSPN-----HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEM 906
      : |      |      : : : | :      ||||| ||||| | :| :      :||:::
Db      826 DPNSNPKAIMGDIQMAHQNLMLDPMGSMSEVPPKVPNREASLYSPSTLPRNSPTKRVDV 885

Qy      907 HHSSSY---GVDYKRSYPTNSLTRSHQATTLKRNTNTSSNSSHLSRNQSFGRGD-NPPPA 962
      :      : : :| | || | | : : : | || |      || | | || | |
Db      886 PTPPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRGGYMPPTPT 943

Qy      963 PQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDPVPPKPSF 1016
      :|| ||      | | :|      ||||: :| |      | :||| ||||| ||||| |||||
Db      944 GAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSNGTLPRTLGLKRTPSLKPDPVPPKPSF 996

Qy      1017 APLSTSMKP 1025
      | : |::|
Db      997 VPQTPSVRP 1005

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RESULT 13

Q9P249

```

ID   Q9P249          PRELIMINARY;          PRT;  1022 AA.
AC   Q9P249;
DT   01-OCT-2000   (TrEMBLrel. 15, Created)
DT   01-OCT-2001   (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2003   (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein KIAA1479 (Fragment).
GN   KIAA1479.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20277482; PubMed=10819331;
RA   Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human
RT   genes.XVII.The complete sequences of 100 new cDNA clones from brain
RT   which code for large proteins in vitro.";
RL   DNA Res. 7:143-150(2000).
DR   EMBL; AB040912; BAA96003.2; -.
DR   GO; GO:0007275; P:development; IEA.
DR   InterPro; IPR003659; Plexin-like.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF01403; Sema; 1.
DR   SMART; SM00423; PSI; 1.
DR   SMART; SM00630; Sema; 1.
KW   Hypothetical protein.

```

FT NON TER 1 1
SQ SEQUENCE 1022 AA; 114372 MW; BE4FBD5EA02C69C4 CRC64;

Query Match 42.5%; Score 2314; DB 4; Length 1022;
Best Local Similarity 45.4%; Pred. No. 1.8e-179;
Matches 494; Conservative 155; Mismatches 292; Indels 148; Gaps 26;

```
QY      1 MRSEALLLYFTLL---HFAGAGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQRHRLD 57
      || | | || ||| ||:: :||:|||| | :| | :| ||||
Db      12 MRVFLLCAYILLMVSQLRVSPFEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD 69

QY      58 IQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDEC 117
      |::: : |||| | | :||::: | : ||||:|||| | : | |||||
Db      70 FQLMLKIRDTLYIAGRDQVYTVNLNEMPKTEVIPNKKLTWRSRQQDRENCAMKGKHKDEC 129

QY     118 HNFIVKVLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF 177
      ||||| : :||: :||| ||||| || ||: || | :| ||:||||:|: | ||||
Db     130 HNFIVKVFVRNDEMVFVCGTNAFNPFCRYRLSTLEYDGEIISGLARCPFDARQTNVALF 189

QY     178 ADGKLYSATVTDFLAIDAVIYRSLGESPTLRVTVKHDSKWLKEPYFVQAVDYGDIYFFFR 237
      ||||| |||| | |||||:| : |||:|:||||:||||:| : ||:|:| ||||
Db     190 ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYFFFR 249

QY     238 EIAVEYNTMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQ 297
      ||||:| :|| | : ||:::||||| ||||| ||||| ||||| ||||:|
Db     250 EIAVEHNNLGKAVYSRVARICKNDMGGSQRVLEKHWTSFLKARLNCSVPGDSFFYFDVLQ 309

QY     298 AVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
      :||:|:| || | :| | ||||| ||: | || | || |||||:| || ||
Db     310 SITDIIQINGIPTVVGVTQNLNIPGSAVCAFSMDIEKVFKEGRFKEQKTPDSVWTAVP 369

QY     358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
      ::||| |||| | | | :||:|:|:| |||| || | : || :| ||
Db     370 EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSFIKSHPLMDSAVPPIADEPWFTKTRVR 429

QY     418 YRLTKIAVDTAAGPYQNHTVTVFLGSEKGIILKFLARIGNSGF-LNDSLFLLEMSVYNSEK 476
      |||| |:| :|||:|:|:| || |:| ||: | | |||: |||: || |
Db     430 YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPFSLNDSVLLEEIEAYNHAK 487

QY     477 CSYDGVEDKRIMGMQLDRASSSLYAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWI 536
      || : |||::: |||: :|||:|:|:| |||:| |||:||||| |||:
Db     488 CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSCCKKSCIASRDPYCGWL 547

QY     537 KEGGACSHLSPNSRLT-----FEQDIERGNTDGLGDCHNSFVALNGHSSSL 582
      : |:| :| | : ||| | || | ||||
Db     548 SQ-GSCGRVTPGMLLLTEDFFAFHNHSAEGYEQDTEFGNTAHLGDCHG----- 594

QY     583 LPSTTTSDSTAQEGYESRGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGH 642
      : |: : | :|
Db     595 -----VRWE--VQSGES----- 604

QY     643 DQLVPVTLIAIAVILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRRGSMSS 701
      |:| : :| | ||:| :|: || | ||: : | : | | |
Db     605 NQMVMHNVLITCVFAAFVLGAFIAGVAVYCYRDMFVRKNRKI--HKDAESAQSCTDSSGS 662

QY     702 VTKLSGLFG----DTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPT 757
      ||:| | : | | : | |: |: :| |||
```

Db 663 FAKLNGLFDSPVKEYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPT 722

Qy 758 PESTPTLQQRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVV 817
 ||||| | || : | : : : | | : | | || | |||| : |

Db 723 PESTPVLHQKTLQAMKSHSEKAHGH--GASRKETPQFFPSSPPPHSPL--SHGHIPSAIV 778

Qy 818 LPITQQGYQHEY-----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLS 860
 || | : : | | | : | || : : || :

Db 779 LPNATHDYNTSFSNSNAHKAEEKLQNI DHPLTKSSSKRDHRRSVDSRNTL--NDLLKHLN 836

Qy 861 SKSPN-----HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEM 906
 : | | : : : | : ||||| ||||| | : : | : : || : :

Db 837 DPNNSPKAIMGDIQMAHQNLMLDPMGSMSEVPPKVPNREASLYSPSTLPRNSPTKRVDV 896

Qy 907 HHSSSY---GVDYKRSYPTNSLTRSHQATT LKRNTNTSSNSSHL SRNQSFGRGD-NPPPA 962
 : : : : | | | | : : : | | | | | | | | | | | |

Db 897 PTPPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRGGYMP TPT 954

Qy 963 PQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSLKRTPSLKPDVPPKPSF 1016
 : || || | | : | |||| : : | | | : ||||| ||||| |||||

Db 955 GAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSNGTLPR TGLKRTPSLKPDVPPKPSF 1007

Qy 1017 APLSTSMKP 1025
 | : | : |

Db 1008 VPQTPSVRP 1016

RESULT 14

Q80TD0

ID Q80TD0 PRELIMINARY; PRT; 1009 AA.

AC Q80TD0;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE MKIAA1479 protein (Fragment).

GN MKIAA1479.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=22579291; PubMed=12693553;

RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,

RA Nakajima D., Nagase T., Ohara O., Koga H.;

RT "Prediction of the coding sequences of mouse homologues of KIAA gene:

RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous

RT cDNAs identified by screening of terminal sequences of cDNA clones

RT randomly sampled from size-fractionated libraries.";

RL DNA Res. 10:35-48(2003).

DR EMBL; AK122515; BAC65797.1; -.

DR InterPro; IPR001627; Sema.

DR Pfam; PF01403; Sema; 1.

DR SMART; SM00630; Sema; 1.

FT NON_TER 1 1

SQ SEQUENCE 1009 AA; 112808 MW; 7509F0B67332316B CRC64;


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Qy      769 KPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE 828
      : | : : : | | : | | | | : | | |
Db      721 LQAMKSHSEKAHSH--GASRKEHPQFFPSSPPPHSPL--SHGHIPSAIVLPNATHDYNTS 776

Qy      829 Y-----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPN----- 865
      : : | | | : | | : : | : |
Db      777 FSNNAHKAIEKKLQSMDDHPLTKSSSKREHRRSVDSRNTL--NDLLKHLNDPNSNPKAILG 834

Qy      866 --HGVNLVENLD-----SLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSY---GV 914
      | : | | : | | | | | | | : | : : | : : : :
Db      835 EIHMAHQTLMLDPVGPMAEVPPKVPNREASLYSPSTLPRNSPTKRVDVPTTPGVPMTSL 894

Qy      915 DYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGD-NPPAPQRVDSIQVHS 973
      : : | | | | : : : | | | | | | | | | : | |
Db      895 ERQRGYHKNSSQR-HSISAVPK-NLNSPNGVLLSRQPSMNRGGYMPPTGAKVDYIQ--- 949

Qy      974 SQPSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDPVPPKPSFAPLSTSMKP 1025
      | | : | | | : | | : | | | | | | | | | | : | : : |
Db      950 ----GTPVSVHLQPSLSRQSSYTSNGTLPRTLGLKRTPSLKPDPVPPKPSFVPQTTSVRP 1003

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RESULT 15

Q96JU9

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ID   Q96JU9      PRELIMINARY;          PRT;   418 AA.
AC   Q96JU9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein FLJ14961.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA   Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA   Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA   Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK027867; BAB55418.1; -.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF01403; Sema; 1.
DR   SMART; SM00630; Sema; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   418 AA;  47415 MW;  2E49A3F6C0564307 CRC64;

```

```

Query Match      40.6%;  Score 2213;  DB 4;  Length 418;
Best Local Similarity  100.0%;  Pred. No. 7.3e-172;
Matches 415;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

```

```

Qy      62 MIMNGTLYIAARDHIYTVDIDTSHTTEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFI 121
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MIMNGTLYIAARDHIYTVDIDTSHTTEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFI 60

```

Qy 122 KVLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGK 181
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 KVLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGK 120

Qy 182 LYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAV 241
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 LYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAV 180

Qy 242 EYNTMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTD 301
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 EYNTMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTD 240

Qy 302 VIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDERV 361
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 VIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDERV 300

Qy 362 PKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLT 421
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 PKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLT 360

Qy 422 KIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEK 476
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 KIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEK 415

Search completed: March 24, 2004, 13:16:25
 Job time : 75.9691 secs

OM protein - protein search, using sw model

Run on: March 24, 2004, 13:07:38 ; Search time 20.5626 Seconds
 (without alignments)
 2608.241 Million cell updates/sec

Title: US-09-856-681A-2
 Perfect score: 5450
 Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	5450	100.0	1030	1	SM6A_HUMAN	Q9h2e6 homo sapien
2	4346.5	79.8	888	1	SM6A_MOUSE	O35464 mus musculu
3	2013.5	36.9	888	1	SM6B_HUMAN	Q9h3t3 homo sapien
4	1997	36.6	887	1	SM6B_RAT	O70141 rattus norv
5	1995	36.6	886	1	SM6B_MOUSE	O54951 mus musculu
6	1515.5	27.8	930	1	SM6C_HUMAN	Q9h3t2 homo sapien
7	1493.5	27.4	931	1	SM6C_MOUSE	Q9wtm3 mus musculu
8	1491	27.4	960	1	SM6C_RAT	Q9wtl3 rattus norv
9	971.5	17.8	730	1	SM1A_SCHAM	Q26473 schistocerc
10	932.5	17.1	771	1	SM1A_DROME	Q24322 drosophila
11	858	15.7	772	1	SM3A_RAT	Q63548 rattus norv
12	853	15.7	772	1	SM3A_MOUSE	O08665 mus musculu
13	852.5	15.6	771	1	SM3A_HUMAN	Q14563 homo sapien
14	845	15.5	712	1	SM1A_TRICF	Q26972 tribolium c
15	845	15.5	778	1	SZ1B_BRARE	Q9w686 brachydanio
16	845	15.5	860	1	SZ1A_BRARE	Q9w7j1 brachydanio
17	839.5	15.4	772	1	SM3A_CHICK	Q90607 gallus gall

18	830	15.2	1074	1	SM5A_HUMAN	Q13591	homo sapien
19	826	15.2	749	1	SM3B_HUMAN	Q13214	homo sapien
20	825.5	15.1	1077	1	SM5A_MOUSE	Q62217	mus musculu
21	803	14.7	748	1	SM3B_MOUSE	Q62177	mus musculu
22	803	14.7	764	1	SMZ2_BRARE	Q9w6g6	brachydanio
23	797	14.6	777	1	SM3D_HUMAN	O95025	homo sapien
24	793.5	14.6	761	1	SM3D_CHICK	Q90663	gallus gall
25	789	14.5	712	1	SM1A_CAEEL	Q17330	caenorhabdi
26	770.5	14.1	1093	1	SM5B_HUMAN	Q9p283	homo sapien
27	766	14.1	1093	1	SM5B_MOUSE	Q60519	mus musculu
28	762.5	14.0	706	1	SM2A_DROME	Q24323	drosophila
29	762	14.0	775	1	SM3E_HUMAN	O15041	homo sapien
30	752	13.8	751	1	SM3C_CHICK	O42236	gallus gall
31	751	13.8	861	1	SM4D_MOUSE	O09126	mus musculu
32	750.5	13.8	697	1	SM2A_SCHGR	Q9xzc8	schistocerc
33	749	13.7	785	1	SM3F_HUMAN	Q13275	homo sapien
34	744.5	13.7	785	1	SM3F_MOUSE	O88632	mus musculu
35	739	13.6	775	1	SM3E_MOUSE	P70275	mus musculu
36	737	13.5	751	1	SM3C_MOUSE	Q62181	mus musculu
37	735.5	13.5	862	1	SM4D_HUMAN	Q92854	homo sapien
38	733.5	13.5	785	1	SM3E_CHICK	O42237	gallus gall
39	733	13.4	751	1	SM3C_HUMAN	Q99985	homo sapien
40	700.5	12.9	766	1	SMZ7_BRARE	Q9yhx4	brachydanio
41	692	12.7	834	1	SM4C_MOUSE	Q64151	mus musculu
42	681	12.5	832	1	SM4B_HUMAN	Q9npr2	homo sapien
43	671	12.3	761	1	SM4A_HUMAN	Q9h3s1	homo sapien
44	664	12.2	776	1	SM4F_RAT	Q9z143	rattus norv
45	658	12.1	777	1	SM4F_MOUSE	Q9z123	mus musculu

ALIGNMENTS

RESULT 1

SM6A_HUMAN

ID SM6A_HUMAN STANDARD; PRT; 1030 AA.
 AC Q9H2E6; Q9P2H9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 6A precursor (Semaphorin VIA) (Sema VIA) (Semaphorin 6A-1)
 DE (SEMA6A-1).
 GN SEMA6A OR KIAA1368.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND INTERACTION WITH EVL.
 RX MEDLINE=20564339; PubMed=10993894;
 RA Klostermann A., Lutz B., Gertler F., Behl C.;
 RT "The orthologous human and murine semaphorin 6A-1 proteins
 RT (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated
 RT phosphoprotein-like protein (EVL) via a novel carboxyl-terminal
 RT zyxin-like domain."
 RL J. Biol. Chem. 275:39647-39653(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XVI.
 RT The complete sequences of 150 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 7:65-73(2000).
 CC -!- FUNCTION: Can act as repulsive axon guidance cues. May play a role
 CC in channeling sympathetic axons into the sympathetic chains and
 CC controlling the temporal sequence of sympathetic target
 CC innervation (By similarity).
 CC -!- SUBUNIT: Active as a homodimer or oligomer. Interacts with EVL.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9H2E6-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9H2E6-2; Sequence=VSP_007113;
 CC Note=No experimental confirmation available;
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; AF279656; AAG29378.1; -.
 DR EMBL; AB037789; BAA92606.1; ALT_INIT.
 DR Genew; HGNC:10738; SEMA6A.
 DR MIM; 605885; -.
 DR GO; GO:0030424; C:axon; NAS.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0008580; F:cytoskeletal regulator activity; NAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0006915; P:apoptosis; NAS.
 DR GO; GO:0007411; P:axon guidance; NAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; NAS.
 DR GO; GO:0007399; P:neurogenesis; NAS.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 1030 SEMAPHORIN 6A.
 FT DOMAIN 19 649 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 650 670 POTENTIAL.
 FT DOMAIN 671 1030 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 56 491 SEMA.

FT	DOMAIN	792	819	PRO-RICH.
FT	CARBOHYD	33	33	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	49	49	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	65	65	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	282	282	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	434	434	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	461	461	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSP LIC	576	576	N -> NDISTPLPDNEMSYNTVY (in isoform 2).
FT				/FTId=VSP_007113.
SQ	SEQUENCE	1030 AA;	114368 MW;	A57B79C10AEC4B34 CRC64;

Query Match 100.0%; Score 5450; DB 1; Length 1030;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPI	ISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Db	1	MRSEALLLYFTLLHFAGAGFPEDSEPI	ISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS	RQADVDTCRMKGKHKDECHNF	120
Db	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS	RQADVDTCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPF	GDEFSGMARCPYDAKHANVALFADG	180
Db	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPF	GDEFSGMARCPYDAKHANVALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240	
Db	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240	
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300	
Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300	
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360	
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360	
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420	
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420	
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480	
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480	
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG	540	
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG	540	
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600	
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600	
Qy	601	GGMLDWKHL L D S P D S T D P L G A V S S H N H Q D K K G V I R E S Y L K G H D Q L V P V T L L A I A V I L A F V	660	

Db	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVLPVTLIAIVILAFV	660
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	720
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERN	780
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQ	840
Db	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQ	840
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Qy	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDNPP	960
Db	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDNPP	960
Qy	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	1020
Db	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	1020
Qy	1021	TSMKPNDACT	1030
Db	1021	TSMKPNDACT	1030

RESULT 2

SM6A_MOUSE

ID SM6A_MOUSE STANDARD; PRT; 888 AA.

AC O35464;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Semaphorin 6A precursor (Semaphorin VIA) (Sema VIA) (Semaphorin 6A-1)

DE (SEMA6A-1) (Semaphorin Q) (Sema Q).

GN SEMA6A OR SEMAQ.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97348468; PubMed=9204478;

RA Zhou L., White F.A., Lentz S.I., Wright D.E., Fisher D.A.,

RA Snider W.D.;

RT "Cloning and expression of a novel murine semaphorin with structural

RT similarity to insect semaphorin I.";

RL Mol. Cell. Neurosci. 9:26-41(1997).

RN [2]

RP INTERACTION WITH EVL.

RX MEDLINE=20564339; PubMed=10993894;

RA Klostermann A., Lutz B., Gertler F., Behl C.;

```

RT  "The orthologous human and murine semaphorin 6A-1 proteins
RT  (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated
RT  phosphoprotein-like protein (EVL) via a novel carboxyl-terminal
RT  zyxin-like domain.";
RL  J. Biol. Chem. 275:39647-39653(2000).
CC  -!- FUNCTION: Can act as repulsive axon guidance cues. May play a role
CC      in channeling sympathetic axons into the sympathetic chains and
CC      controlling the temporal sequence of sympathetic target
CC      innervation.
CC  -!- SUBUNIT: Active as a homodimer or oligomer. Interacts with EVL.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- TISSUE SPECIFICITY: Particularly high levels in spinal cord,
CC      cerebellum, metencephalon, superior and inferior colliculus,
CC      diencephalon, olfactory bulb and eye.
CC  -!- DEVELOPMENTAL STAGE: Temporally and spatially regulated during
CC      development.
CC  -!- SIMILARITY: Belongs to the semaphorin family.
CC  -!- SIMILARITY: Contains 1 Sema domain.
CC  -----
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CC  -----
DR  EMBL; AF030430; AAB86408.1; -.
DR  MGD; MGI:1203727; Sema6a.
DR  GO; GO:0030424; C:axon; NAS.
DR  GO; GO:0016020; C:membrane; NAS.
DR  GO; GO:0005515; F:protein binding; IPI.
DR  GO; GO:0006915; P:apoptosis; NAS.
DR  GO; GO:0007411; P:axon guidance; NAS.
DR  InterPro; IPR003659; Plexin-like.
DR  InterPro; IPR001627; Sema.
DR  Pfam; PF01403; Sema; 1.
DR  SMART; SM00423; PSI; 1.
DR  SMART; SM00630; Sema; 1.
KW  Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW  Developmental protein.
FT  SIGNAL          1      18      POTENTIAL.
FT  CHAIN           19     888      SEMAPHORIN 6A.
FT  DOMAIN          19     649      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM        650     670      POTENTIAL.
FT  DOMAIN          671     888      CYTOPLASMIC (POTENTIAL).
FT  DOMAIN          56     491      SEMA.
FT  DOMAIN          792     819      PRO-RICH.
FT  CARBOHYD        33      33      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        49      49      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        65      65      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD       282     282      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD       434     434      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD       461     461      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE       888 AA;  99075 MW;  C7094FC2BB345C57 CRC64;

```

Query Match

79.8%; Score 4346.5; DB 1; Length 888;


```

Db      781 QNIINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVVA 840
Qy      840 QMALEDQAATLEYKTIKEHLSSKS 863
        |||||:|
Db      841 QMALEDQAATLEYKTIKEHLSSES 864

```

RESULT 3

SM6B_HUMAN

```

ID      SM6B_HUMAN      STANDARD;      PRT;      888 AA.
AC      Q9H3T3; Q9NRK9;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Semaphorin 6B precursor (Semaphorin Z) (Sema Z).
GN      SEMA6B OR SEMAZ.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RC      TISSUE=Brain;
RA      Kimura T., Ishida H.;
RL      Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORM 2).
RX      MEDLINE=21248680; PubMed=11350127;
RA      Correa R.G., Sasahara R.M., Bengtson M.H., Katayama M.L.H.,
RA      Salim A.C.M., Brentani M.M., Sogayar M.C., de Souza S.J.,
RA      Simpson A.J.G.;
RT      "Human semaphorin 6b.";
RL      Genomics 73:343-348(2001).
CC      -!- FUNCTION: MAY PLAY A ROLE IN BOTH PERIPHERAL AND CENTRAL NERVOUS
CC      SYSTEM DEVELOPMENT (BY SIMILARITY).
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Comment=Additional isoforms seem to exist;
CC      Name=1;
CC      IsoId=Q9H3T3-1; Sequence=Displayed;
CC      Name=2; Synonyms=6B.1;
CC      IsoId=Q9H3T3-2; Sequence=VSP_006044, VSP_006045;
CC      -!- SIMILARITY: Belongs to the semaphorin family.
CC      -!- SIMILARITY: Contains 1 Sema domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB022433; BAB20669.1; -.
DR      EMBL; AF216389; AAF87661.1; -.
DR      Genew; HGNC:10739; SEMA6B.

```

DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 888 SEMAPHORIN 6B.
 FT DOMAIN 26 603 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 604 624 POTENTIAL.
 FT DOMAIN 625 888 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 238 547 SEMA.
 FT DOMAIN 661 674 POLY-GLY.
 FT DOMAIN 750 753 POLY-LEU.
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 471 517 LSVFLEEFETYRPDRCGRPGGGETGQRLLSLELDAASGGLL
 FT AAFPRC -> RVCQVGHACRVCVHERRSWWPQRPGRWLSRR
 FT WGFQKARGPPRCRLGV (in isoform 2).
 FT /FTId=VSP_006044.
 FT VARSPLIC 518 888 Missing (in isoform 2).
 FT /FTId=VSP_006045.
 FT CONFLICT 30 30 D -> E (IN REF. 2).
 SQ SEQUENCE 888 AA; 95270 MW; 6FFB44D6828C70CB CRC64;

Query Match 36.9%; Score 2013.5; DB 1; Length 888;
 Best Local Similarity 45.3%; Pred. No. 3.6e-122;
 Matches 424; Conservative 129; Mismatches 241; Indels 141; Gaps 20;

Qy 5 ALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQR--HRLDIQMIM 62
 |||| || | ||| |:|:: :| ||||| ||| | :|| ::
 Db 12 ALLLLLLLLGGAGHLFPEDPPPLSVAPRDYLNHYPVFGSGPGRLTPAEGADDLNIQRLV 71
 Qy 63 IMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNFIK 122
 :| ||:| ||::| |::: :|: :|||:| :|:: ||||| : || ||:|
 Db 72 RVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGECRNFVK 131
 Qy 123 VLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKL 182
 ||| ::| ||||:|||| | || :||:| || ||||| ||||| |||||:| |
 Db 132 VLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDGML 191
 Qy 183 YSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVE 242
 ::||| ||||| |||||: ||||| ||||| ||::| :||| |||||:|
 Db 192 FTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREIAME 251
 Qy 243 YNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDV 302
 :| : ||| ||:||||:||| ||||| ||||| ||||| |||||: ||||| |
 Db 252 FNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTGV 311
 Qy 303 IRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDPDERVP 362
 : : || |||| |||| ||||| |||||:|: :|: || |||: |||||:| |||||: |||||


```

RP      SEQUENCE FROM N.A.
RC      STRAIN=Wistar; TISSUE=Brain;
RX      MEDLINE=98087397; PubMed=9427525;
RA      Kikuchi K., Ishida H., Kimura T.;
RT      "Molecular cloning of a novel member of semaphorin family genes,
RT      semaphorin Z.";
RL      Brain Res. Mol. Brain Res. 51:229-237(1997).
CC      -!- FUNCTION: MAY PLAY A ROLE IN BOTH PERIPHERAL AND CENTRAL NERVOUS
CC      SYSTEM DEVELOPMENT.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- DEVELOPMENTAL STAGE: DETECTED IN THE FIRST BRANCHIAL ARCH OF
CC      EMBRYONIC DAY 11 (E11) EMBRYO, AND SUBSEQUENTLY IN THE MYOTOMES
CC      AND THE DORSAL ROOT GANGLIA IN DEVELOPING SOMITES FROM E11.5
CC      THROUGH E13.5, BUT NOT IN THE BRAIN. HOWEVER, AT E15, 18, 21 AND
CC      P0, SEMAZ WAS HIGHLY EXPRESSED IN THE BRAIN.
CC      -!- SIMILARITY: Belongs to the semaphorin family.
CC      -!- SIMILARITY: Contains 1 Sema domain.

```

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DR EMBL; AB000776; BAA25687.1; -.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW Developmental protein.

FT	SIGNAL	1	26	POTENTIAL.
FT	CHAIN	27	887	SEMAPHORIN 6B.
FT	DOMAIN	27	605	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	606	626	POTENTIAL.
FT	DOMAIN	627	887	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	239	549	SEMA.
FT	CARBOHYD	75	75	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	168	168	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	387	387	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	442	442	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	463	463	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	887 AA;	95752 MW;	09543F3F202CD301 CRC64;

Query Match 36.6%; Score 1997; DB 1; Length 887;
Best Local Similarity 42.7%; Pred. No. 4.2e-121;
Matches 433; Conservative 132; Mismatches 260; Indels 190; Gaps 25;

Qy 2 RSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQR--HRLDIQ 59
| | | || |: : |: : :| ||||| ||| | |:|
Db 10 RPALLFLLLLLLLRVTHGLFPDEPPPLSVAPRDYLSHPYVFVGSGPGRLTPAEGAEDLNIQ 69

Qy 60 MIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSROADVDTCRMKGKHKDECHN 119
 :: :| ||:| ||::| |::: | : | : :|||:| :|:| ||||| : || |

Db 70 RVLRVNRTLFIGDRDNLYQVELEPSTSTELRYQRKLTWRSNPSDIDVCRMKGQEGECRN 129

Qy 120 FIKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFAD 179
 |:||| ::: ||||:|||| | || |||: || ||||| |||||:|

Db 130 FVKVLLLRDESTLFVCGSNAFNPICANYSMDTLQLLGDNISGMARCPYDPKHANVALFSD 189

Qy 180 GKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREI 239
 | |:|||||||||||||: ||||| ||||| |:| :|:|||||

Db 190 GMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREI 249

Qy 240 AVEYNTMGKVVFPRAVQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAV 299
 |:|:| : || | ||:||||:| || ||||| |||||:|

Db 250 AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAV 309

Qy 300 TDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDE 359
 | |: : || |:| ||| ||||| |||:| |:| ||:||||:| ||||:|

Db 310 TGVVSLGGRPVILAVFSTPSNSIPGSAVCAFDNMQVAAVFEGRFREQKSPESIWTVPED 369

Qy 360 RVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYR 419
 :||:||||| :| || ||: |||:||||| |||: : || :|:|::

Db 370 QVPRPRPGCCAAPGM--QYNASNALPDEILNFVKTHPLMDEAVPSLGHSPWIVRTLIRHQ 427

Qy 420 LTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLAR--IGNSGFLNDSL FLEEMSVYNSEKC 477
 ||::||| ||:| |:|||| | :||| : || |:||| | :|

Db 428 LTRVAVDVGAGPWGNQTVFLGSEVGTVLKFLVKPNASVSGTTGPSIFLEEFETYRPDRC 487

Qy 478 ---SYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCG 534
 | | ::: :|| || | || ||::||| ||: : | | | |:|||

Db 488 GRSSSAGEWGQRLLSLELDAASGGLLAAPRCVVRVPVARCQLYSGCMKNCIGSQDPYCG 547

Qy 535 WIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQ 594
 | : |:| | | : ||||: :| ||||

Db 548 WAPD-GSCIFLRPGTSATFEQDVSGASTSGLGDC----- 580

Qy 595 EGYESRGGMLDWKHLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPVTLAIA 654
 |::| | || | | :

Db 581 -----TGLLRASLSDDRAGLVSVNLLVTS 604

Qy 655 VILAFVMGAVFSGITV-YCVDHRRKDVAVVQRKEKE--LTHSRGSMSSVTKL----- 705
 : |||:|| | | : | |::| :||:| | | :|:|

Db 605 SVAAFVVGAVVSGFSVGFVGLRERRELA--RRKDKEAILAHGGSEAVLSVSRLGERRGT 662

Qy 706 --SGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT 763
 | | ||:| || | | | : | | |||| |

Db 663 GTGGRGGAGGGPGGPPEALLAPLMQNGW-----TKAALLHGPHDLDSGLLPTPEQTP- 715

Qy 764 LQQKRKPSR-----GSREWERNQNINACTK-----DMPPMGSPVIPTD-- 802
 | ||| |: | | : : |:| : || :|:

Db 716 LPQKRLPTTHPHAHALGPRAWDHSHALLSASASTSLLLLAHTRAPEQPP-----VPTESG 770

Qy 803 -----LPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK 856
 | || :| | | : : | :

Db 771 PESRLCAPRSCRASHPGDFPLTP-----HASPDRRRVVSAPTGPLDSSSVG----- 816

Qy 857 EHLSSKSPNHGVNLVENLDSLP-PKVPQREASL-----GPPGASLSQTGLSKRLEMHHS 909

```

      | | | | | : | | | | | : | |
Db      817 -----DDLPGWSPPATSSLRRPGPHGPPTAALRRT-----HT 849

Qy      910 SSYGV DYKRSYPTNSLTRSHQATTLKRNNNTSSNSSHLSRNQSFGRGD-NPPAP 963
      : | : | | : | | : | |
Db      850 FNSG----EARPGGHRPRRHA-----PADSTHL---LPCGTGERTAPPVP 887

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RESULT 5

SM6B_MOUSE

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ID      SM6B_MOUSE      STANDARD;      PRT;      886 AA.
AC      O54951;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Semaphorin 6B precursor (Semaphorin VIB) (Sema VIB) (Semaphorin N)
DE      (Sema N).
GN      SEMA6B OR SEMAN.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98027184; PubMed=9361278;
RA      Eckhardt F., Behar O., Calautti E., Yonezawa K., Nishimoto I.,
RA      Fishman M.C.;
RT      "A novel transmembrane semaphorin can bind c-src.";
RL      Mol. Cell. Neurosci. 9:409-419(1997).
CC      -!- SUBUNIT: HOMODIMER. BINDS SPECIFICALLY THE SH3 DOMAIN OF THE
CC      PROTOONCOGENE C-SRC.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- TISSUE SPECIFICITY: During development it is expressed in
CC      subregions of the nervous system and is particularly prominent in
CC      muscle. In adulthood, it is expressed ubiquitously.
CC      -!- SIMILARITY: Belongs to the semaphorin family.
CC      -!- SIMILARITY: Contains 1 Sema domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      -----
DR      EMBL; AF036585; AAC00493.1; -.
DR      MGD; MGI:1202889; Sema6b.
DR      InterPro; IPR003659; Flexin-like.
DR      InterPro; IPR001627; Sema.
DR      Pfam; PF01403; Sema; 1.
DR      SMART; SM00423; PSI; 1.
DR      SMART; SM00630; Sema; 1.
KW      Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW      Developmental protein.
FT      SIGNAL      1      26      POTENTIAL.
FT      CHAIN      27      886      SEMAPHORIN 6B.

```

FT	DOMAIN	27	605	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	606	626	POTENTIAL.
FT	DOMAIN	627	886	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	239	549	SEMA.
FT	DOMAIN	751	754	POLY-LEU.
FT	CARBOHYD	75	75	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	387	387	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	442	442	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	463	463	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	886 AA;	95466 MW;	E5F56D125CDA574D CRC64;

Qy	8	LYFTLLHFAGAG---FPEDSEPI SISHGNYTKQYPVFGHKPGRNTTQR--HRLDIQMIM	62
Db	13	LSFFLLLLLLGVTYGLFPPEEPPLSVAPRDYLSHYPVFVGSGPGRLTAAEGAEDLNIQRVL	72
Qy	63	IMNGTLYIAARDHIYTVDDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNFIK	122
Db	73	RVNRTLFIGDRDONLYQVELEPSTSTELRYQRKLTWRSNPDSIDVCRMKGKQEGECRNFEVK	132
Qy	123	VLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKL	182
Db	133	VLLLRDESTLFVCGSNAFNPICANYSMDTLQLLGDSISGMARCPYDPKHANVALFSDGML	192
Qy	183	YSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFFREIAVE	242
Db	193	FTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGS HVYFFFFREIAME	252
Qy	243	YNTMGKVVFPRAVQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVTDV	302
Db	253	FNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGD SHFYFNVLQAVTGV	312
Qy	303	IRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVP	362
Db	313	VSLGGRPVILAVFSTPSNSIPGSAVCAFDMNQVAAVFEGRFREQKSPESIWTPVPEDQVP	372
Qy	363	KPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTK	422
Db	373	RPRPGCCAAPGM--QYNASSALPDEILNFVKTHPLMDEAVPSLGHSPWIVRTLMRHQLTR	430
Qy	423	IAVDTAAGPYQNHTVVFLGSEKGIILKFLAR--IGNSGFLNDSLFL EEMS VYNSEKC---	477
Db	431	VAVDVGAGPWGNQTIVFLGSEAGTVLKLFLVKPNASVSGTTGPSIFLEEFETYRPDRCGRP	490
Qy	478	SYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIK	537
Db	491	SSAGEWGQRLLSLELDAASGGLLAAPRCVVRVPVARCQLYSGCMKNCIGSQDPYCGWAP	550
Qy	538	EGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGY	597
Db	551	D-GSCIFLRPGTSATFEQDVSGASTSGLGDC-----	580

Qy 598 ESRGGLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHQDLVPVTLIAIVIL 657
 Db 581 -----TGLLRASLSDDRAGLVSVNLLVTSSVA 607
 Qy 658 AFVMGAVFSGITV-YCVC DHRRKDVAVVQRKEKE--LTHSRRGSMSSVTKL SGLFGDTQS 714
 Db 608 AFVVGVAVVSGFVGVFWGLRERRELA--RRKDKEAILAHGGSEAVLSVSRL----GERRG 661
 Qy 715 KDP-----KPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTP 762
 Db 662 TGPGRGGAGGGPGGPPEALLAPLMQNGW-----TKAALLHGGPHDLDTGLLPTPEQTP 715
 Qy 763 TLQQKRKP-----SRGSREWERNQNLINACTKDMPPMGSPVIPTDL----PLRASPSH 811
 Db 716 -LPQKRLPTPHPHAHALGSRWDHSHALLSASAS-----TSLLLLAPARASEQ- 762
 Qy 812 IPSVVVLPIITQQGYQHEYVDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGV 868
 Db 763 -PQVPAEPGPE-----SRLCAPRSCRASHPGDFPLTPHASPDORRRVVSAPTGPLDPSVG- 815
 Qy 869 NLVENLDSLP-PKVPQREASL-----GPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYP 921
 Db 816 -----DGLPGPWSPPATSSLRRPGPHGPPTAALRRT-----HTFNSG----EARP 856
 Qy 922 TNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGD-NPPPPAP 963
 Db 857 GGHRPRRHP-----PADSTHL---LPCGTGERTAPPVP 886

RESULT 6

SM6C_HUMAN

ID SM6C_HUMAN STANDARD; PRT; 930 AA.
 AC Q9H3T2; Q8WXT8; Q8WXT9; Q8WXU0; Q96JF8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y).
 GN SEMA6C OR SEMAY OR KIAA1869.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RA Kimura T., Ishida H.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Brain;
 RA Qu X., Zhai Y., Wei H., Zhang C., Xing G., Yu Y., Wu S., Zhang Y.,
 RA Ouyang S., Zhou G., He F.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=21245130; PubMed=11347906;

RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XX.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 8:85-95(2001).
 CC -!- FUNCTION: May be a stop signal for the dorsal root ganglion
 CC neurons in their target areas, and possibly also for other
 CC neurons. May also be involved in the maintenance and remodeling of
 CC neuronal connections (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=Short 1;
 CC IsoId=Q9H3T2-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short 2;
 CC IsoId=Q9H3T2-2; Sequence=VSP_006046, VSP_006047;
 CC Name=3; Synonyms=Long;
 CC IsoId=Q9H3T2-3; Sequence=VSP_006047;
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; AB022434; BAB20670.1; -.
 DR EMBL; AF339152; AAL72098.1; -.
 DR EMBL; AF339153; AAL72099.1; -.
 DR EMBL; AF339154; AAL72100.1; -.
 DR EMBL; AB058772; BAB47498.1; ALT_INIT.
 DR Genew; HGNC:10740; SEMA6C.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 930 SEMAPHORIN 6C.
 FT DOMAIN 25 604 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 605 625 POTENTIAL.
 FT DOMAIN 626 930 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 233 540 SEMA.
 FT DOMAIN 662 667 POLY-PRO.
 FT DOMAIN 752 755 POLY-PRO.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 184 223 Missing (in isoform 2).
 FT /FTId=VSP_006046.
 FT VARSPLIC 586 586 Y -> YVLPGGPGSPGTPSPPSDAHPRPQSSTLGVHTR
 FT (in isoform 2 and isoform 3).

FT /FTId=VSP_006047.
 FT CONFLICT 125 125 I -> V (IN REF. 2; AAL72099).
 FT CONFLICT 252 252 R -> K (IN REF. 1).
 FT CONFLICT 455 455 P -> T (IN REF. 1 AND 3).
 SQ SEQUENCE 930 AA; 99682 MW; 8AF8814ADBC84C88 CRC64;

Query Match 27.8%; Score 1515.5; DB 1; Length 930;
 Best Local Similarity 35.8%; Pred. No. 5.3e-90;
 Matches 380; Conservative 136; Mismatches 356; Indels 189; Gaps 32;

Qy 6 LLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMN 65
 ||| :| | | ||:| |: || | | : | | | :| |
 Db 13 LLLLLSLPH-TQAAFPQDPLPLLISDLQGTSPLSWFRGLEDDAVAAEL-GLDFQRFLLTN 70

Qy 66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNFIKVL 124
 || :||| |::| : | : :| |||:| ||: | :|| |||:|:| |
 Db 71 RTLLVAARDHVFSFDLQAEEEGGLVPNKYLWRSQ--DVENCAVRGKLTDECYNYIRVL 128

Qy 125 LKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYS 184
 : : | |||:|:| ||:| : :| :| || |||:| | :||:|:| | |
 Db 129 VPWDSQTLACGTNSFSPVCRSYGITSLQQEGEELSGQARCPDATQSNVAIFAEGSLYS 188

Qy 185 ATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYN 244
 || || | |||:| || | ||: | :|||:|:| |||:|:|:|:|:|:|:| |
 Db 189 ATAADFQASDAVVYRSLGQPPLRSKYDSKWLREPHFVQALEHGDHVVYFFFREVSVEDA 248

Qy 245 TMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPGDSHFYFNILQAVTDVIR 304
 :|:| | |||:| | ||| | | :| ||| | ||| | ||| | |||:| | :
 Db 249 RLGRVQFSRVARVCKRDMGGSPRALDRHWTSLKLRLNCVPGDSTFYFDVLQALTGPVN 308

Qy 305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDERVPKP 364
 ::|| : | :| ||| | |||:| : :| | | :|||:| | ||| :||| |
 Db 309 LHGRSALFGVFTTQTNSIPGSAVCAFYLDEIERGFEGKFKEQRLDGAWTPVSEDRVPSP 368

Qy 365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA 424
 ||| ||| :::| : ||| | ||| |||:| ||| : :| | | ||:| |
 Db 369 RPGSCAGVGGAALFSSSRDLDPDDVLTFIKAHPLLDPAVPPVTHQP-LLTLTSRALLTQVA 427

Qy 425 VDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVED 484
 || |||:| ||:| || | :|| | | || : : |||: | : :||
 Db 428 VDMAGPHSNITVMFLGSNDGTVLKVLPPGGRSGG-PEPILLEEIDAYSPARCSGKRTAQ 486

Qy 485 --KRIMGMLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWKEGGAC 542
 :||:|:| | :||| | :| || || || | :||:|:|:| ||| | |
 Db 487 TARRIIGLELDTEGHRLFVAFSGCIVYLP LSRCARHGACQRSCLASQDPYCGWHSSRG-C 545

Qy 543 SHLSPNSRLTFEQDIERGNTDGL--GDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR 600
 : : :| || : : ||| : :| : |
 Db 546 VDIRSGGTDVDQ---AGNQESMEHGDCQDG-----ATGSQSGPGDSAY--- 586

Qy 601 GGMLDWKHLSDSPDSTDPLGAVSSHNHQQDKKGVIRESYLKGHQDLVPVTLIAIVILAFV 660
 || | : : ||:| | :| ||
 Db 587 -----GVERRDLPPASASRSVPIPLLLASVAAFA 615

Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRG-----SMSSVTKL SGL 708
 :|| ||:| | | | | | ||| | :| :| | |
 Db 616 LGASVSGLLVSCAC--RR-----AHRRRGKDIETPGLPRPLSLRSLARLHG- 659

Qy 709 FGDTQSKDPKP--EAILTPLMHNGKLIATPGNTAKMLIKADQHHLDTALPTPESTPTLQQ 766
 | : | : | | : : | | : | | | | | | |
 Db 660 -GGPEPPPPSKDGDVQTPQLYTTFPPPEGVPPP-----ELACLPTPESTPELPV 709

Qy 767 KRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSH-----IPSVVVLPIIT 821
 | : | | | | | : | | : | | : | |
 Db 710 KHLRAAGD-PWEWNQNRNNA-----KEGPGRSRGGHAAGGPAPRVLVLP-- 752

Qy 822 QQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHL----SSKSPNHGVNLVENLDS- 876
 | | | | : | | : | | : | | | | | |
 Db 753 -----PPPGCPGQ-----AVEVTTLEELLRYLHGPQPPRKGAEPPAPLTSR 793

Qy 877 -LPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLK 935
 | | | : | | | : | | : | | | | | | |
 Db 794 ALPPE--PAPALLGGPSRPHCASPLRLDV-----PPEGRCASAPA---- 833

Qy 936 RNNTNSSNSSHL----SRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPS--- 988
 | : : | | | | | | | | | | | | | |
 Db 834 -RPALSAPAPRLGVGGGRRLLPFSGHRAPPALLTRV-----PSGGPSRYSGGPGKHL 883

Qy 989 --LNAYNSLTRSGLKRTPSLKPDPVPPKPSF-APLSTSMKPN 1026
 | | | | | : | | | | | | | |
 Db 884 LYLGRPEGYRGRALKRVDVEKPKQLSLKPPLVGPSSRQAVPN 924

RESULT 7

SM6C_MOUSE

ID SM6C_MOUSE STANDARD; PRT; 931 AA.

AC Q9WTM3;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y).

GN SEMA6C OR SEMAY.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=99160821; PubMed=10049528;

RA Kikuchi K., Chedotal A., Hanafusa H., Ujimasa Y., de Castro F.,

RA Goodman C.S., Kimura T.;

RT "Cloning and characterization of a novel class VI semaphorin,

RT semaphorin Y.";

RL Mol. Cell. Neurosci. 13:9-23(1999).

CC -!- FUNCTION: May be a stop signal for the dorsal root ganglion

CC neurons in their target areas, and possibly also for other

CC neurons. May also be involved in the maintenance and remodeling of

CC neuronal connections (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the semaphorin family.

CC -!- SIMILARITY: Contains 1 Sema domain.

CC

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 CC or send an email to license@isb-sib.ch).

 DR EMBL; AB013729; BAA76294.1; -.
 DR MGD; MGI:1338032; Sema6c.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 931 SEMAPHORIN 6C.
 FT DOMAIN 26 605 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 606 626 POTENTIAL.
 FT DOMAIN 627 931 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 234 541 SEMA.
 FT DOMAIN 663 669 POLY-PRO.
 FT DOMAIN 754 757 POLY-PRO.
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 931 AA; 99537 MW; B0D99D594209F125 CRC64;

Query Match 27.4%; Score 1493.5; DB 1; Length 931;
 Best Local Similarity 35.7%; Pred. No. 1.4e-88;
 Matches 374; Conservative 145; Mismatches 353; Indels 177; Gaps 32;

Qy 6 LLLYFTLLHFAGAGFPEDSEPISSISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIN 65
 ||| : | | | ||: | : | | : : || | : : |
 Db 13 LLLLLSSLPQAQAAPQDPTPLLTSDLQGASPSWFRGLEDDAVAAEL-GLDFQRFLTLN 71
 Qy 66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVL 124
 || : |||||::: | : : | |||: | : | : || | |||:|:|
 Db 72 RTLLVAARDHVFSFDLQAQEEGGLVLPNKFLTWRSQ--DMENCAVRGKLTDECYNYIRVL 129
 Qy 125 LKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYS 184
 : | | ||||:| | : | : : | : | || ||||:| | : ||:|:| ||
 Db 130 VPWNSQTLLACGTNSFSMPCRSYGITSLQQEGEELSGQARCPFDATQSTVAIFAEGSLYS 189
 Qy 185 ATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVEYN 244
 || || | |||:|||| | ||: | |||||:|:| || |::|::| |||||:|
 Db 190 ATAADFQASDAVVYRSLGPQPPLRS AKYDSKWLREPHFVYALEHGEHVYFFFREVSVEDA 249
 Qy 245 TMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIR 304
 :|:| | |||:| | |||| | : : ||||| ||||| |||||:|:| :
 Db 250 RLGRVQFSRVARVCKRDMGGSPRALDRHWTSFLKLRNLCSVPGDSTFYFDVLQSLTGPN 309
 Qy 305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDERVPKP 364
 :|| : | : | ||||| ||| : || | | : ||||:| | |||| :||| |
 Db 310 LHGRSALFGVFTTQTNSIPGSAVCAFYLLDDIERGFEGKFKEQSRSLDGAWTPVSEDKVPSP 369
 Qy 365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA 424
 ||| ||| : :||: | || | ||| |||:| ||| :|| | | |||:

Db 370 RPGSCAGVGAAASFSSSQDLPPDVLFFIKAHPLLDPAVPPATHQP-LLTLTSRALLTQVA 428

Qy 425 VDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVED 484
 || |||::| ||:|||| | :|| | | :: : |||: |: :|| |

Db 429 VDMAGPHRNTTVLFLGSNDGTVLKVLPP-GGQSLGSEPIVLEEIDAYSHARCS--GKRS 485

Qy 485 ----KRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540
 :||:|::|| |:||| |:: : | || ||| |:::|:| ||||| : |

Db 486 PRAARRIIGLELDTEGHRLFVAFPGCIVYLSLSRCARHGACQRSCLASLDPYCGWHRSRG 545

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYE-S 599
 | | | || | | | : | | | | | | | | | | | | | | | |

Db 546 CMSIRGP-----GGTD-----VDLTGNQES-----TEHGDCQDGATGS 578

Qy 600 RGGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLKQHDQLVPVTLTLLAIVILAF 659
 : | | : | | | | | | | | | | | | | | | | | | | |

Db 579 QSGPGDSAY-----GVRDLSPASASRSIPIPLLLACVAAAF 615

Qy 660 VMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDKPKP 719
 :|| ||: | | | || : :||: ||: | : | : | | | | |

Db 616 ALGASVSGLLVSCAC--RRAN----RRRSKDIETPGLPRPLSLRSLARLHGGGPEPPPPP 669

Qy 720 ---EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSRE 776
 :| || :: | | : :| ||||:| | | | : |

Db 670 KDGDAAQTPQLYTTFLPPPDGGSPP-----ELACLTPETTPPELPVKHLRASGG-P 719

Qy 777 WERNQNLINACT-KDMPPMGSPVIPTDLP---LRASPHIPSVVVLPTITQQ---GYQH-- 827
 || ||| || || | | | | : | | | | | | : | | |

Db 720 WEWNQNGNNASEGPRPPRGCSGAGGPAPRVLVRRPPPGCPGQAVEVTLEELLRYLHGP 779

Qy 828 -----EYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENL 874
 : :| || | | | | | | | | | | | | | | | |

Db 780 QPPRGKSEPLASAPFTSRPPASEPGASLFVD-----SSPMRDPVPPL-RL 824

Qy 875 DSLPPK----VPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQ 930
 | :||: | :| | | | | | | | | | | | | | | |

Db 825 D-VPPEGKRAAPSGRPALSAPAPRLG-VGGSRL-----PFPT-----HR 862

Qy 931 ATTLKRNTNTSSNSSHLNRNQSFGRGDNPPAPQRVDS--IQVHSSQPSGQAVTVSRQPS 988
 | | | | | | | | | | | | | | | | | | | | |

Db 863 A-----PPGLLTRVPSSGGPARYSSGGPGRHLLYLGR-PE 894

Qy 989 LNAYNSLTRSGLKRTPSLKPDV--PPKPS 1015
 : || | :| | || : ||:|:

Db 895 GHRGRSLKRVDVKSPSPKPLASPPQPA 923

RESULT 8

SM6C_RAT

ID SM6C_RAT STANDARD; PRT; 960 AA.

AC Q9WTL3; Q9WTM6;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y).

GN SEMA6C OR SEMAY.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS SEMA Y-L AND SEMA Y-S).
 RC STRAIN=Sprague-Dawley; TISSUE=Muscle;
 RX MEDLINE=99160821; PubMed=10049528;
 RA Kikuchi K., Chedotal A., Hanafusa H., Ujimasa Y., de Castro F.,
 RA Goodman C.S., Kimura T.;
 RT "Cloning and characterization of a novel class VI semaphorin,
 RT semaphorin Y.";
 RL Mol. Cell. Neurosci. 13:9-23(1999).
 CC -!- FUNCTION: SHOWS GROWTH CONE COLLAPSING ACTIVITY ON DORSAL ROOT
 CC GANGLION (DRG) NEURONS IN VITRO. MAY BE A STOP SIGNAL FOR THE DRG
 CC NEURONS IN THEIR TARGET AREAS, AND POSSIBLY ALSO FOR OTHER
 CC NEURONS. MAY ALSO BE INVOLVED IN THE MAINTENANCE AND REMODELING OF
 CC NEURONAL CONNECTIONS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Sema Y-L;
 CC IsoId=Q9WTL3-1; Sequence=Displayed;
 CC Name=Sema Y-S;
 CC IsoId=Q9WTL3-2; Sequence=VSP_006048;
 CC -!- TISSUE SPECIFICITY: Expressed in many regions of the developing
 CC nervous system, probably in neurons and their precursors, but also
 CC in nonneural tissue such as immature muscle and dermis. In adult,
 CC strong expression in the skeletal muscle and moderate expression
 CC in the brain, where cerebellum shows the highest expression. Also
 CC expressed in almost all areas of the CNS.
 CC -!- DEVELOPMENTAL STAGE: DETECTED AT E12 AND FOUND AT MARKEDLY
 CC INCREASED LEVELS AT E15 AND E18 IN BOTH THE HEAD AND THE BODY. AT
 CC BIRTH THE LEVEL DECREASES SIGNIFICANTLY.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; AB000817; BAA76293.2; -.
 DR EMBL; AB014074; BAA76295.1; -.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 960 SEMAPHORIN 6C.
 FT DOMAIN 24 635 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 636 656 POTENTIAL.
 FT DOMAIN 657 960 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 234 541 SEMA.

FT	DOMAIN	693	699	POLY-PRO.
FT	DOMAIN	783	786	POLY-PRO.
FT	CARBOHYD	69	69	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	285	285	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	436	436	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	586	617	Missing (in isoform Sema Y-S).
FT				/FTId=VSP_006048.
SQ	SEQUENCE	960 AA;	102610 MW;	C88293C5607E6086 CRC64;

Query Match 27.4%; Score 1491; DB 1; Length 960;
 Best Local Similarity 35.1%; Pred. No. 2.1e-88;
 Matches 374; Conservative 149; Mismatches 363; Indels 180; Gaps 32;

Qy	6	LLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMMN	65
		: : : : : :	
Db	11	LLLLLLSLPQAQTAFPDPIPLLTSDLQGTSPSSWFRGLEDDAVAAEL-GLDFQRFLTLN	69
Qy	66	GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVL	124
		: : : : : : : : : : :	
Db	70	RTLLVAARDHVFSFDLQAQEEGGLVPNKFLTWSQ--DMENCAVRGKLTDECYNYIRVL	127
Qy	125	LKKND DALFVCGTNAFNPSCRNYKMDTLEPFGEDEFSGMARCPYDAKHANVALFADGKLYS	184
		: : : : : : : : : : : :	
Db	128	VPWDSQTLLACGTNSFSPVCRSYGITSLQQEGEELSGQARCPDATQSTVAISAEGSLYS	187
Qy	185	ATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYN	244
		: : : : : : : : : :	
Db	188	ATAADFQASDAVVYRSLGPQPPLRSKYDSKWLREPHFVYALEHGDHVFYFFFREVSVEDA	247
Qy	245	TMGKVVFPRAVQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIR	304
		: : : : : : : :	
Db	248	RLGRVQFSRVARVCKRDMGGSPRALDRHWTSLKLRLNCSVPGDSTFYFDVLQSLTGPNV	307
Qy	305	INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDERVPKP	364
		: : : : : : : : :	
Db	308	LHGRSALFGVFTTQTNSIPGSAVCAFYLDIERGFEGKFKEQRSLDGAWTPVSEDKVPSP	367
Qy	365	RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA	424
		: : : : : : :	
Db	368	RPGSCAGVGAAALFSSSQDLPPDVLFLFIKAHPLLDPAVPPATHQP-LLTLTSRALLTQVA	426
Qy	425	VDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVED	484
		: : : : : : :	
Db	427	VDGMAGPHRNTTVLFLGSNDGTVLKVLPP-GGQSLGPEPIILEEIDAYSHARCS--GKRS	483
Qy	485	----KRIMGQLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWKEGG	540
		: : : : : : : : : :	
Db	484	PRAARRIIGLELDTEGHRLFVAFFPGCIVYLSLRCARHGACQRSCLASLDPYCGWHFRFG	543
Qy	541	ACSHLSPNSRLTFEQDIE-RGNTDGL--GDCHNSFVALN---GHSSSL-----PSTTT	588
		: : : : : : :	
Db	544	CVNIRGPGG-----TDVDLTGNQESMEHGDCQDGATGSQSGPGDSAYVLLGPGPSPETPS	598
Qy	589	SDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSSHNHQDKKGVIRESYLKGHDLVPV	648
		: : : : :	
Db	599	SPSDAHPGPQS-----STLGA-----HTQGVRRDLSPASASRSIPI	634

Qy 649 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGL 708
 || | || :|| ||: | | | || : :|| :|| :| :| :|
 Db 635 PLLLACVAAAFALGASVSGLLVSCAC--RRAN---RRRSKDIETPGLPRPLSLRSLARL 688

Qy 709 FGDTQSKDPKP---EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQ 765
 | | | :| || :| | | : :| ||||:| | |
 Db 689 HGGGPEPPPPPKDGDAAQTPQLYTTFLPPPEGGSPP-----ELACLPTPETTPELP 739

Qy 766 QKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLP---LRASPSHIPSVVLPITQ 822
 | : | || || | | | | :| | | | | |
 Db 740 VKHLRASGG-PWEWNQNGNNASEGPRPRGCSAAGGPAPRVLVRPPPGCPGQEEVEVTTL 798

Qy 823 Q---GYQH-----EYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSP 864
 : | | : :| || | | | | || |
 Db 799 EELLRYLHGPPQPPRKGEPLASAPFTSRPPASEPGAALFVD-----SSPMP 844

Qy 865 NHGVNLVENLDSLPP-----KVPQREASLGPPGASLSQTGLSKRLEMHHSSSYG 913
 | :|| | :| | | :| | :||
 Db 845 R-----DCVPPLRLDVPDPDGKRAAPSGRPALSAPAPRLGVSG-SRRL----- 885

Qy 914 VDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSHL SRNQSFGRGDNPPAPQRVDS--IQV 971
 :|| | :| | | || || |
 Db 886 -----PFPT-----HRA-----PPGLLTRVPSGGPSR 907

Qy 972 HSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDV--PPKPS 1015
 :| | : :| | : || | :| || : ||:|
 Db 908 YSGGPGRHLLYLGR-PDGHGRSLKRVDVKSPKPLATPPQPA 952

RESULT 9

SM1A_SCHAM

ID SM1A_SCHAM STANDARD; PRT; 730 AA.

AC Q26473;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Semaphorin 1A precursor (Semaphorin-I) (Sema I) (Fasciclin IV).

GN SEMA-1A OR FAS4.

OS Schistocerca americana (American grasshopper).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.

OX NCBI_TaxID=7009;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=93040225; PubMed=1418998;

RA Kolodkin A.L., Matthes D.J., O'Connor T.P., Patel N.H., Admon A.,

RA Bentley D., Goodman C.S.;

RT "Fasciclin IV: sequence, expression, and function during growth cone

RT guidance in the grasshopper embryo.";

RL Neuron 9:831-845(1992).

CC -!- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: DYNAMICALLY EXPRESSED ON A SUBSET OF AXON

CC PATHWAYS IN THE DEVELOPING CNS AND ON CIRCUMFERENTIAL BANDS OF

CC EPITHELIAL CELLS IN DEVELOPING LIMB BUDS.

CC -!- SIMILARITY: Belongs to the semaphorin family.

```

CC      -!- SIMILARITY: Contains 1 Sema domain.
CC      -----
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CC      -----
DR      EMBL; L00709; AAA29808.1; -.
DR      PIR; JH0798; JH0798.
DR      InterPro; IPR003659; Plexin-like.
DR      InterPro; IPR002165; Plexin_repeat.
DR      InterPro; IPR001627; Sema.
DR      Pfam; PF01437; PSI; 1.
DR      Pfam; PF01403; Sema; 1.
DR      SMART; SM00423; PSI; 1.
DR      SMART; SM00630; Sema; 1.
KW      Signal; Developmental protein; Transmembrane; Glycoprotein;
KW      Neurogenesis.
FT      SIGNAL          1      20      POTENTIAL.
FT      CHAIN           21     730      SEMAPHORIN 1A.
FT      DOMAIN          21     630      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        631     651      POTENTIAL.
FT      DOMAIN          652     730      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          215     515      SEMA.
FT      DOMAIN          217     222      POLY-PHE.
FT      CARBOHYD         44      44      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD         71      71      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        163     163      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        267     267      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        360     360      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        539     539      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE       730 AA;  81214 MW;  6D625946E7F8E57F CRC64;

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Query Match          17.8%; Score 971.5; DB 1; Length 730;
Best Local Similarity 34.4%; Pred. No. 4.8e-55;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

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```

Qy      8 LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQR-----HRLDIQMI 61
      | : || | : | | | | | | | | | | | | | | | | : ::
Db      11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFGLGNESHKDHFKLL 54

Qy      62 MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN 119
      : : | : || : | : : | || : : : | | | : | : || : | : |
Db      55 EKDHNSLLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy      120 FIKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV 174
      : | : || | : || : : || || : | || : | | : | | : | :
Db      110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFPDPHNST 165

Qy      175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYF 234
      | : : : | : || || | | : || | || : | | | | || : : | : | : |
Db      166 AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERS DLKQLNAPNFVNTMEYNDFFIFF 220

Qy      235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFN 294

```

Db	221	:: : : : :: :	
		FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQFGDR-WTSFLKSRLNCSVPGDYPPFYFN	279
QY	295	ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD	350
		: : : : : : :: :	
Db	280	EQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSILESFDGPFKEQETMN	339
QY	351	STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW	410
		: : : : : :	
Db	340	SNWLAVPSLKVPEPRPGQCVND-----SRTLDPVSVNFVKSHITLMDEAVPAFFTRPI	391
QY	411	FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN-----	461
		: : : : : : : : : : :	
Db	392	LIRISLQYRFTKIAVDQQV RTPDG--KAYDVLFIGTDDGKVIKAL----NSASFDSSDTV	445
QY	462	DSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG	519
		: : : : : :: : : : :	
Db	446	DSVVIEELQVLP-----PGVPVKNLVVRMDGDDSKLVVSDDEILAIKLHRCGSDKIT	499
QY	520	KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL	575
		:: : : : : : : : : : :	
Db	500	NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV-	557
QY	576	NGHSSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQ	628
		: : : : : : : : : : :	
Db	558	----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA	610
QY	629	DKKGVIRESYLKGHDQLVPV----TL-LAI-----AVILAFVMGAVFS	666
		: : : : :: : :	
Db	611	GSK-----LPSSQEKLPITYAETLTIAIVTSCLGALVVGFI SGFLFS	652

RESULT 10

SM1A_DROME

ID SM1A_DROME STANDARD; PRT; 771 AA.

AC Q24322;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Semaphorin 1A precursor (Semaphorin-I) (Sema I).

GN SEMA-1A OR DSEMA-I OR CG18405.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=94094332; PubMed=8269517;

RA Kolodkin A.L., Matthes D.J., Goodman C.S.;

RT "The semaphorin genes encode a family of transmembrane and secreted

RT growth cone guidance molecules.";

RL Cell 75:1389-1399(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED BY SUBSETS OF NEURONS AND MUSCLES.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSION BEGINS AROUND STAGE 10, PRIMARILY
 CC IN THE DEVELOPING CNS. IN STAGE 16 EMBRYOS, IT IS EXPRESSED AT
 CC HIGHEST LEVELS THROUGHOUT THE CNS, AND WEAK EXPRESSION IS SEEN IN
 CC PORTIONS OF THE PERIPHERAL NERVOUS SYSTEM, MOST CLEARLY IN THE
 CC LATERAL SENSORY CLUSTERS.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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CC -----
 DR EMBL; L26082; AAA88789.1; -.
 DR EMBL; AE003621; AAF52696.1; -.
 DR FlyBase; FBgn0011259; Sema-1a.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Developmental protein; Transmembrane; Glycoprotein;
 KW Neurogenesis.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 771 SEMAPHORIN 1A.
 FT DOMAIN 21 608 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 609 629 POTENTIAL.
 FT DOMAIN 630 771 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 210 519 SEMA.
 FT DOMAIN 689 694 POLY-PRO.
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 771 AA; 86935 MW; 752E7DD516F32DA5 CRC64;

Query Match 17.1%; Score 932.5; DB 1; Length 771;
 Best Local Similarity 35.0%; Pred. No. 1.7e-52;
 Matches 219; Conservative 106; Mismatches 213; Indels 87; Gaps 20;

Qy 67 TLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNFIKVLK 126
 :| | ||: :: : | :: :| | | : | :||| :: | |:|:::
 Db 57 SLLIGARNTVFNLISI-----HDLVEQQRLVWTSPEDDTKMCLVKGKDEEACQNYIRIMVV 111
 Qy 127 KNDDALFVCGTNAFNPSCRNYKMD----TLEPFGDEFSGMARCPYDAKHANVALFADGKL 182
 : | | | | | | :| | | : | | | | :| : :: | :|
 Db 112 PSPGRLFVCGTNSFRPMCNTYIISDSNYTLEA---TKNGQAVCPYDPRHNSTSVLADNEL 168
 Qy 183 YSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVE 242
 || || || | :||| |:| ::|| | || : ||::| | | ||
 Db 169 YSGTVADFSGSDPIIYRE-----PLQTEQYDSLNLNAPNFVSSFTQGDFVYFFFRETAVE 223
 Qy 243 YNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPGDSHFYFNILQAVTDV 302
 : || :: |||: || | | : |||||: ||||: || | || :| : ::
 Db 224 FINCGKAIYSRVARVCKWDKGGPHR-FRNRWTSFLKSRLNCSIPGDYPFYFNEIQSASNL 282
 Qy 303 IR----INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPD 358
 : :: |:| | | | | | | : : || | | :| | || :
 Db 283 VEGQYGSMSSKLIYGVENTPSNSIPGSAVCAFALQDIADTFEGQFKEQTGINSNWLVPNN 342
 Qy 359 ERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRY 418
 :|| |||| | : | || | | | | | | ||| ||: |:| :|| |
 Db 343 AKVPDPRPGSC-----HNSRALPDPTLNFIKTHSLMDENVPAFFSQPILVRTSTIY 394
 Qy 419 RLTKIAVD-----TAAGPYQNHTVVFLGSEKGIILKFL-ARIGNSGFLNDSLFLLEMSVYN 473

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      | :| | | |   | | : : | :| :| : | :|   | : :| | : |
Db      395 RFTQIAVDAQIKTPGG--KTYDVIFVGTDHGKIIKSVNAESADSADKVTSSVVEEIDVLT 452

QY      474 SEKCSYDGVEDKRIM-GMQLDRASSSLY-----VAFSTCVIKVPLGRC--ERHGKCKKT 524
      : : : | : | | | :   |   :   : | : : | | | : :   | :
Db      453 KS-----EPIRNLEIVRTMQYDQPKDGSYDDGKLIIVTDSQVVAIQLHRCHNDKITSCE- 507

QY      525 CIASRDYPYCGWIKEGGAC-SHLSPN--SRLTFEQDIERGNTDGLGDCHNSFVALNGHSSS 581
      | : | :| | | | | | | | | | :|   | | : : |   | : :
Db      508 CVALQDPYCAWDKIAGKCRSHGAPRWLEENYFYQNVATGQ-----HAAC 551

QY      582 LLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKG 641
      : | : | | | | | | | | | | | | | | | | : : |
Db      552 PSGKINSKDANAGEQKGFNRDM----DLLDS-----RRQSKDQEIIDNIDKN 594

QY      642 HDQLVPVTLIAIAVILAFVMGAVFS 666
      : : :   : : | : | : | |
Db      595 FEDIINAQYTVETLVMMAVLGSIIFS 619

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RESULT 11

SM3A_RAT

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ID      SM3A_RAT          STANDARD;          PRT;    772 AA.
AC      Q63548;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Semaphorin 3A precursor (Semaphorin III) (Sema III).
GN      SEMA3A.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Wistar; TISSUE=Brain;
RX      MEDLINE=97073089; PubMed=8915837;
RA      Giger R.J., Wolfer D.P., De Wit G.M.J., Verhaagen J.;
RT      "Anatomy of rat semaphorin III/collapsin-1 mRNA expression and
RT      relationship to developing nerve tracts during neuroembryogenesis.";
RL      J. Comp. Neurol. 375:378-392(1996).
CC      -!- FUNCTION: MAY BE INVOLVED IN GUIDING GROWING AXONS TOWARDS THEIR
CC      TARGETS BY FORMING A MOLECULAR BOUNDARY THAT INSTRUCTS AXONS TO
CC      ENGAGE IN THE FORMATION OF SPECIFIC NERVE TRACTS. BINDS TO
CC      NEUROPILIN.
CC      -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC      -!- DEVELOPMENTAL STAGE: AT E-11, EXPRESSION WAS RESTRICTED TO THE
CC      OLFACTORY PIT, THE BASAL AND ROSTRAL SURFACE OF THE TELENCEPHALIC
CC      VESICLE, THE EYE ANLAGE, THE EPITHELIUM OF RATHKE'S POUCH, AND
CC      SOMITES. AT LATER DEVELOPMENTAL STAGES, IT WAS WIDELY DISTRIBUTED
CC      IN NEURONAL AS WELL AS IN MESENCHYMAL AND EPITHELIAL STRUCTURES
CC      OUTSIDE THE NERVOUS SYSTEM. AFTER BIRTH, MESENCHYMAL LEVELS
CC      DECREASED RAPIDLY AND EXPRESSION BECAME RESTRICTED TO SPECIFIC
CC      SETS OF NEURONS IN THE CNS. IN THE MATURE CNS, IT IS DETECTABLE IN
CC      MITRAL CELLS, NEURONS OF THE ACCESSORY BULB AND CEREBRAL CORTEX,
CC      CEREBELLAR PURKINJE CELLS, AS WELL AS A SUBSET OF CRANIAL AND
CC      SPINAL MOTONEURONS.

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CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
 CC third of the protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; X95286; CAA64607.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 772 SEMAPHORIN 3A.
 FT DOMAIN 240 538 SEMA.
 FT DOMAIN 577 665 IG-LIKE C2-TYPE.
 FT DOMAIN 728 770 ARG/LYS-RICH (BASIC).
 FT DISULFID 650 723 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 772 AA; 88808 MW; 240907812FF9F2D2 CRC64;

Query Match 15.7%; Score 858; DB 1; Length 772;
 Best Local Similarity 32.3%; Pred. No. 1.1e-47;
 Matches 209; Conservative 104; Mismatches 251; Indels 84; Gaps 20;

Qy 47 GRNTTQRHRLDIQMIMMNGT-----LYIAARDHIYTVDIDT 83
 |:| |:| :::| ||:|:||||: ::
 Db 25 GKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHIFSFL-- 82
 Qy 84 SHTEEIYCSKKLTWKSQRQADVDTCRMKGKH-KDECHNFIKVLKKNDDALFVCGTNAFNP 142
 | :|:| |:| || || ||||| |:| ||| ||:|
 Db 83 ---VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP 139
 Qy 143 SCR-----NYKMDTLEPFGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLAIDA 195
 | : : |:| :||| |:| ||:|||| |:| :|
 Db 140 ICTYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLLIDGELYSGTAADFMRGRDF 199
 Qy 196 VIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGK 248
 |:|:| |:| :||:| |:| |:| |:| ||| |:| :||
 Db 200 AIFRTLGHHPHPIRTEQHDNRWLNDRPFISAHLPESDNPEDDKVYFFFRENAIDGEHSGK 259

Qy	249	VVFPRAVQVCKNDMGGSQRVLEKQWTSFLKARLNCSPVG----	DSHFYFNILQAVTDVIR	304
Db	260	ATHARIGQICKNDFGG-HRSLVNKWTTFLKARLICSVPGPNGIDTHF----	DELQDVFL	313
Qy	305	INGRD---VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER		360
Db	314	MNSKDPKNPIVYGVTTSNIFKGSAVCMYSMSDVRVFLGPYAHRDGPENYQWVPY-QGR		372
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL		420
Db	373	VPYPRPGTCP-SKTEGGFDSTKDLPPDDVITFARSHPAMYNPVFPINNRPIMIKTDVNYQF		431
Qy	421	TKIAVDTAAGPYQNHTVVFVLGSEKGIILKFLARIGNSGFLNDSLFLFLEEMSVYNSEKCSYD		480
Db	432	TQIVVDRVDAEDGQYDVMFIGTVDVGTVLKVVSVPKETWHDL EEVLLEEMTVFR-----		484
Qy	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGWIKEGG		540
Db	485	--EPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECLARDPYCAW--DGS		540
Qy	541	ACSHLSPNS-RLTFEQDIERGNTDGLGDC-----HNSFVALNGHS--SSILPSTTTSDST		592
Db	541	SCSRYFPTAKRRTRRQDIRNG--DPLTHCSDLQHHDNH---HGHSLEERIIYGVENSSTF		595
Qy	593	AQEGYESRGGMLDWKHLSDSPDSTDPLGAVSSSHNHQDKKGVIRESYLK		640
Db	596	LECSPKSQRALVYWQFORNEDRKEEI-RVG DHIIRTEQGLLLRSLOK		642

RA Yaqi T.;

RT "Disruption of semaphorin III/D gene causes severe abnormality in
 RT peripheral nerve projection.";
 RL Neuron 19:519-530(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kimura T., Fishman M.C.;
 RT "cDNA sequence of mouse collapsin/semaphorin III.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 107-772 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=95267432; PubMed=7748562;
 RA Messersmith E.K., Leonardo E.D., Shatz C.J., Tessier-Lavigne M.,
 RA Goodman C.S., Kolodkin A.L.;
 RT "Semaphorin III can function as a selective chemorepellent to pattern
 RT sensory projections in the spinal cord.";
 RL Neuron 14:949-959(1995).
 CC -!- FUNCTION: Play a role in growth cones guidance. May function to
 CC pattern sensory projections by selectively repelling axons that
 CC normally terminate dorsally.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN EMBRYONIC DEVELOPMENT
 CC (E11) IN DISTINCT REGIONS OF THE NEUROECTODERM AND MESODERM.
 CC EXPRESSION BECAME MORE EXTENSIVE AT LATER STAGES.
 CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
 CC third of the protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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CC -----
 DR EMBL; X85993; CAA59985.1; -.
 DR EMBL; D85028; BAA19773.1; -.
 DR EMBL; L41541; AAL77611.1; -.
 DR EMBL; BC057588; AAH57588.1; -.
 DR EMBL; L40484; AAA73934.1; -.
 DR PIR; I48747; I48747.
 DR PIR; I58169; I58169.
 DR MGD; MGI:107558; Sema3a.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 772 SEMAPHORIN 3A.
 FT DOMAIN 240 538 SEMA.
 FT DOMAIN 579 665 IG-LIKE C2-TYPE.
 FT DOMAIN 728 770 ARG/LYS-RICH (BASIC).
 FT DISULFID 650 723 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 193 193 D -> N (IN REF. 5).
 FT CONFLICT 207 207 H -> D (IN REF. 1).
 FT CONFLICT 253 253 D -> G (IN REF. 1).
 FT CONFLICT 352 352 F -> L (IN REF. 5).
 FT CONFLICT 403 403 A -> G (IN REF. 1).
 FT CONFLICT 571 572 QH -> ED (IN REF. 1).
 FT CONFLICT 616 620 EDRKE -> RRSKR (IN REF. 1).
 FT CONFLICT 623 623 R -> K (IN REF. 5).
 SQ SEQUENCE 772 AA; 88799 MW; E89A08528B10AEC3 CRC64;

Query Match 15.7%; Score 853; DB 1; Length 772;
 Best Local Similarity 32.2%; Pred. No. 2.3e-47;
 Matches 208; Conservative 102; Mismatches 257; Indels 78; Gaps 18;

Qy 47 GRNTTQRHRLDIQMIMIMNGT-----LYIAARDHIYTVDDIDT 83
 |:| |:| :::| ||: |:|::: ::
 Db 25 GKNNVPRCLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHIFSFL-- 82
 Qy 84 SHTEEIYCSKKLTWKSQRQADVDCRMKGKH-KDECHNFIKVLLKKND DALFVCGTNAFNP 142
 | :|: | | : | | || ||| | | : ||| ||:|
 Db 83 ---VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLEAYNQTHLYACGTGAFHP 139
 Qy 143 SCR-----NYKMDTLEPFGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLAIDA 195

```

      |      :: | : |      :| : ||| |      :| ||: ||| | ||: |
Db      140 ICTYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLLIDGELYSGTAADFMGRDF 199

Qy      196 VIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGK 248
      |:|:| |      :| | :|||:| | :| | : |      | :||| | | :| : | |
Db      200 AIFRTLGHHPIRTEQHDSRWLNDPRFISAHLIPESDNPEDDKVYFFFRENAIDGEHSGK 259

Qy      249 VVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSPVG----DSHFYFNILQAVTDVIR 304
      |: | :||| | | | | :| | :||| | | | | | | | | :| |      : | |
Db      260 ATHARIGQICKNDFGG-HRSLVNKWTTFKARLICSVPGPNGIDTHF-----DELQDVFL 313

Qy      305 INGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
      :| :|      :| | :| | | | | | | | | | :| :| :| :| :| :| |
Db      314 MNSKDPKNPIVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPYQWVPY-QGR 372

Qy      361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
      || ||| | | | :| :| :| :| | | :| :| | | | | | | | :| | | :|
Db      373 VPYPRPGTCP-SKTFGGFDSTKDLRDDVITFARSHPAMYNPVFPINNRPIMIKTDVNYQF 431

Qy      421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
      |:| | |      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      432 TQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSVPKETWHDLEEVLEEMTVFR----- 484

Qy      481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGG 540
      | | | :| | | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      485 --EPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAW--DGS 540

Qy      541 ACSHLSPNS-RLTFEQDIERGNTDGLGDCHNSFVALNGHSSSL----LPSTTTSDSTAQE 595
      :| | | :| | | | | | | :| | | | | :| :| :| :| :| :| :|
Db      541 SCSRYFPTAKRRTRRQDIRNG--DPLTHCSDLQHHDNHHGPSLEERIYGVENSSTFLEC 598

Qy      596 GYESRGGMLDWKHLDDSPDSTDPLGAVSSHNHQDKKGVIRESYLK 640
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      599 SPKSQRALVYWQFQRRNEDRKEEI-RMGDHIIRTEQGLLLRSLQK 642

```

RESULT 13

SM3A_HUMAN

ID SM3A_HUMAN STANDARD; PRT; 771 AA.

AC Q14563;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Semaphorin 3A precursor (Semaphorin III) (Sema III).

GN SEMA3A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal brain;

RX MEDLINE=94094332; PubMed=8269517;

RA Kolodkin A.L., Matthes D.J., Goodman C.S.;

RT "The semaphorin genes encode a family of transmembrane and secreted

RT growth cone guidance molecules.";

RL Cell 75:1389-1399(1993).

RN [2]
 RP SEQUENCE OF 1-37 FROM N.A.
 RA Woessner J., Minx P., Hinds K., Strowmatt C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 39-182 FROM N.A.
 RA Rohlfing T., Tin-Wollam A.M., Duckels G.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH
 CC CONES. COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWTH CONES
 CC BY A MOTILITY-INHIBITING MECHANISM. BINDS TO THE COMPLEX
 CC NEUROPILIN-1/PLEXIN-1 (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
 CC third of the protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 DR EMBL; L26081; AAA65938.1; -.
 DR EMBL; AC004451; -; NOT_ANNOTATED_CDS.
 DR EMBL; AC004848; AAC78622.1; -.
 DR PIR; D49423; D49423.
 DR Genew; HGNC:10723; SEMA3A.
 DR MIM; 603961; -.
 DR GO; GO:0005576; C:extracellular; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 771 SEMAPHORIN 3A.
 FT DOMAIN 240 538 SEMA.
 FT DOMAIN 580 664 IG-LIKE C2-TYPE.
 FT DOMAIN 727 769 ARG/LYS-RICH (BASIC).
 FT DISULFID 649 722 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 590 590 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 771 AA; 88889 MW; 9985F8D3EAED8456 CRC64;

Query Match 15.6%; Score 852.5; DB 1; Length 771;
 Best Local Similarity 32.1%; Pred. No. 2.5e-47;
 Matches 208; Conservative 106; Mismatches 250; Indels 83; Gaps 20;

```

Qy      44 HKPGRNTTQRHRLDIQMIMIMNGT-----LYIAARDHIYTV 80
      :: |:| | :| : :: | ||: |:|:|:|: |
Db      22 YQNGKNNVPRLKLSYKEMLESNNVITFENGLANSSSYHTFLLDEERSRLYVGAKDHIFSFD 81

Qy      81 IDTSHTEEIYCSKKLTWKSQADVDTCRMKGKH-KDECHNFIKVLKKND DALFVCGTNA 139
      : | :|: | | :| || || ||||| | |: ||| |
Db      82 L-----VNIKDFQKIVVPVSYTRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGA 136

Qy     140 FNPSCR-----NYKMDTLEPFGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLA 192
      |:| | :|: | : :| : ||| | :| ||:| | ||:
Db     137 FHPICTYIEIGHHPEDNIFKLENSHFENGGRGKSPYDPKLLTASLLIDGELYSGTAADF MG 196

Qy     193 IDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNT 245
      | |:|:| | :| :||:| | :| | : | | :| ||||| |::
Db     197 RDFAIFRTLGHHPHPIRTEQHDRWLNDPKFISAHLISESDNPEDDKVYFFFRENAIDGEH 256

Qy     246 MGKVVFPFVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPG----DSHFYFNILQAVTD 301
      || |: |:| || || | | :||:| ||||| ||||| |:| : |
Db     257 SGKATHARIGQICKNDFGG-HRSLVNKWTTF LKARLICSVPGPNGIDTHF-----DELQD 310

Qy     302 VIRINGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
      | :| :| || |:| | |||| | | |: || | : : |: | |
Db     311 VFLMNFKDPKNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPYQWVPY- 369

Qy     358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
      ||| |||| | | : : : : ||| : | :|| | | : ||| :| |
Db     370 QGRVPYPRPGTCP-SKTFGGFDSTKDLPDVVITFARSHPAMYNPVFPMNNRPVVIKTDVN 428

Qy     418 YRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKC 477
      |: |:| || : |:|:|:| :| || : : : : |||:|:
Db     429 YQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSIPKETWYDLEEV LLEEMTVFR---- 484

Qy     478 SYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIK 537
      | | |:| ||: : | :|| ||: :| | :| |||| |
Db     485 -----EPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAW-- 537

Qy     538 EGGACSHLSPNS-RLTFEQDIERGNTDGLGDC----HNSFVALNGHS--SSLLPSTTTSD 590
      :| ||| | : | | ||| | | | | :| : :||| : : |
Db     538 DGSACSRYPFTAKRRTRRQDIRNG--DPLTHCSDLHHDNH---HGHSPEERIIYGVENSS 592

Qy     591 STAQEGYESRGGMLDWKHL LSPDSTDP LGAVSSSHNHQDKKGVIRE 637
      : : :|: :| : : : : | | : :|:| |
Db     593 TFLECSPKSQRALVYWQFQRRNEERKEEI-RVDDHII RTDQGLLLRS 638

```

RESULT 14

SM1A_TRICF

ID SM1A_TRICF STANDARD; PRT; 712 AA.

AC Q26972;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Semaphorin 1A precursor (Semaphorin-I).

GN SEMA-1A OR TSEMA-I.
 OS Tribolium confusum (Confused flour beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tribolium.
 OX NCBI_TaxID=7071;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=94094332; PubMed=8269517;
 RA Kolodkin A.L., Matthes D.J., Goodman C.S.;
 RT "The semaphorin genes encode a family of transmembrane and secreted
 RT growth cone guidance molecules.";
 RL Cell 75:1389-1399(1993).
 CC -!- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; L26080; AAA16609.1; -.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Developmental protein; Transmembrane; Glycoprotein;
 KW Neurogenesis.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 712 SEMAPHORIN 1A.
 FT DOMAIN 21 601 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 602 622 POTENTIAL.
 FT DOMAIN 623 712 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 213 506 SEMA.
 FT DOMAIN 470 473 POLY-VAL.
 FT DOMAIN 612 616 POLY-VAL.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 712 AA; 79751 MW; C0734FE5B9C09FE3 CRC64;

Query Match 15.5%; Score 845; DB 1; Length 712;
 Best Local Similarity 28.9%; Pred. No. 6.8e-47;
 Matches 230; Conservative 130; Mismatches 270; Indels 166; Gaps 30;

Qy 12 LLHFAGAGFPEDSEPI-----SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMN- 65
 |: | |: | : |: ::| | | :||

Db 12 LIALCHAWMPDSSSKLINHFKSVESKSFT-----GNATFPDH-----FIVLNQ 54
 Qy 66 --GTLYIAARDHIYTVDI-DTSHTEEIYCSKKLWKSQRQADVDCRMKGKHKDECHNFIK 122
 : : : | : : | : | : : : | | | : | | : | : | :
 Db 55 DETSILVGGRNRVYNLSIFDLSEK----GGRIDWPSSDAHGQLCILKGKTDDDCQNYIR 110
 Qy 123 VLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGD-EFSGMARCPYDAKHANVALFADGK 181
 : | : | | | : | | | : : | | : | | : : | : : : | :
 Db 111 ILYSSEPGLVICGTNSYKPLCRTYAFKEGKYLVEKEVEGIGLCPYNPEHNSTSVSYNGQ 170
 Qy 182 LYSATVTDFLAIDAVIYRSLGESPTLRVTKHDSKWLKEPYFVQAVDYGDIYFFFREIAV 241
 | : | | | | | : | | | | | | | | : | | | | : | : | | | |
 Db 171 LFSATVADFSGGDPLIYRE-----PQTELSDLKQLNAPNFVNSVAYGDYIFFFFYRETAV 225
 Qy 242 EYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSSHFYFNILQAVTD 301
 | | | | : | | : | | : | | : : | | | | | | : | : | : | : |
 Db 226 EYMNCCKVIYSRVARVCKDDKGGPHQSRDR-WTSFLKARLNCSIPGEYPFYFDEIQSTSD 284
 Qy 302 VI--RINGRD---VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPV 356
 : : | | | : : : | | | | | : | | | | | | | | : : : | | |
 Db 285 IVEGRYNSDDSKKIIYGILTPVNAIGGSAICAYQMADILRVFEGSFKHQETINSNWLVP 344
 Qy 357 PDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMV 416
 | | : | | | | : : | | : | | | | | : : | : : | : : :
 Db 345 PQNLVPEPRPGQCVRDSRI-----LPDKNVNFIKTHSLMED-VPALFGKPVILVRVSL 395
 Qy 417 RYRLTKIAVDTAAGPYQNH--TVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNS 474
 : | | | | | | : | | : | : : | : | : | : | : | : | :
 Db 396 QYRFTAITVDPQVKTINNQYLDVLYIGTDDGKVLK----- 430
 Qy 475 EKCSYDGVEDKRIMGMQLDRASSSLYAFSTCV-----IKVP----- 511
 : : : | : | : | : : : : : : : : : : : : : : : :
 Db 431 -----AVNIPKRHAKALLYRKYRTSVHPHGAPVKQLKIAPGYKVVVVGKDEI 478
 Qy 512 ----LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTF-EQDIERN----- 561
 | | : | | : : | : | : | : : | : : : | | : | : :
 Db 479 RLANLNHCASKTRC-KDCVELQDPHCAWDAKQNLCSIDTVTSYRFLIQDVVRGDDNKCW 537
 Qy 562 ---TDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDP 618
 | | | | | | | : : | : : : | | | | : | : | : | :
 Db 538 SPQTDKKTVIKNK-----PSEVENEIT-----NSIDEKDL----DSSDP 572
 Qy 619 LGAVSSHNHQDKKGVIRESYLKG---HDQLVPVT--LLAIAVILAFVMGA---VFSGITV 670
 | : | | | : : | | | | | | | : : : | : : : | : : : |
 Db 573 LIKTGLDDSDCDPV-SENSIGGCAVRQQLVIYTAGTLHIVVVVVSIVGLFSWLVSGLSV 631
 Qy 671 YCV--CDHRRKDVAVVQRKE--KELTHSRGMS-SVTKLSGLFGDTQSKDPKPEAILTP 725
 : | : : : : : : | : : : | : : | | | | : | : :
 Db 632 FAKFHSDSQYPEAPFIEQHNHLERLSANQTGYLTFRANKAVNLVVKVSSSTPRPKKNLD 691
 Qy 726 LMHNGKLATPGNTAKM 741
 : : : | : | :
 Db 692 VSKDLNIASDGTLOKI 707

ID SZ1B_BRARE STANDARD; PRT; 778 AA.
 AC Q9W686;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin Z1B precursor (Semaphorin 1B) (Sema-Z1B).
 GN SEMAZ1B OR SEMA3AB.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99425174; PubMed=10495275;
 RA Roos M., Schachner M., Bernhardt R.R.;
 RT "Zebrafish semaphorin Z1b inhibits growing motor axons in vivo."
 RL Mech. Dev. 87:103-117(1999).
 CC -!- FUNCTION: MIGHT NORMALLY INFLUENCE THE MIDSEGMENTAL PATHWAY CHOICE
 CC OF THE VENTRALLY EXTENDING MOTOR AXONS BY CONTRIBUTING TO A
 CC REPULSIVE DOMAIN IN THE POSTERIOR SOMITE.
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN RHOMBOMERES THREE AND FIVE, AND
 CC IN THE POSTERIOR HALF OF NEWLY FORMED SOMITES WHICH IS AVOIDED BY
 CC VENTRALLY EXTENDING MOTOR AXONS.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 DR EMBL; AF083382; AAD28103.1; -.
 DR ZFIN; ZDB-GENE-991209-6; sema3ab.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 778 SEMAPHORIN Z1B.
 FT DOMAIN 241 539 SEMA.
 FT DOMAIN 579 668 IG-LIKE C2-TYPE.

